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!!SEQUENCE\_LIST 1.0  
(Nucleotide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-1 check: 7546 from:

FROMIG of: /home/obryen/ree455/olig/us08836455.seq  
sequence 1, application us/08836455

general information:  
applicant: chatterjee, malaya  
applicant: foon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: geneseqn: \* Sequences: 240,622 Total-length: 94,065,609 April 18, 1999 13:41

Database Release Information:

Geneseq-NA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

Word-size: 15 Words: 48182 Diagonals: 1,619 Total diagonals: 396,990,246  
Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 29.44

Sequence SeqD Diag Score Width Documentation ..

GENESON:T85149	+	0	435	1	Murine monoclonal anti-idiotypic anti
GENESON:N30165	+	18	345	1	Sequence encoding the leader, variabl
GENESON:Q46084	+	339	306	1	Sequence encoding 520C9 sfv protein.
GENESON:T36880	+	339	306	1	520C9 anti-c-erbB-2 two single chain
GENESON:V63399	+	339	306	1	520C9 sfv DNA sequence. Nucleic acid
GENESON:V21798	+	339	306	1	520C9 anti-c-erbB-2 sfv' dimeric cons
GENESON:Q46086	+	1212	287	1	Sequence encoding G-FTT. New single c
GENESON:Q97507	+	-60	262	1	light chain variable region for monoc
GENESON:Q97504	+	-60	262	1	light chain variable region for monoc
GENESON:Q97510	+	-60	261	1	light chain variable region for monoc
GENESON:T77851	+	6	220	1	Murine anti-human class II monoclonal
GENESON:T85091	+	-60	147	1	Murine monoclonal antibody B9 light ch
GENESON:Q30755	+	0	142	1	ppm-K3. Reconstituted human antibody
GENESON:T87818	+	-60	128	1	Antibody 362 light chain variable reg
GENESON:Q36607	+	0	122	1	Anti-CD4 antibody MT 15.1 light chain
GENESON:T51437	+	32	122	1	Murine MAb SK48-E26 light chain DNA.
GENESON:N90672	+	15	116	1	DNA sequence encoding upprocessed vari
GENESON:Q51229	+	835	115	1	DNA encoding humanised anti-erbB2 spe
GENESON:V20086	+	30	108	1	Consensus DNA sequence of the murine
GENESON:V02198	+	-60	108	1	CDNA for light chain variable region
GENESON:T34816	+	-60	104	1	Humanised anti-CD38 monoclonal antibo
GENESON:T34541	+	21	102	1	Monoclonal anti-idiotypic antibody 3H1
GENESON:T31540	+	21	102	1	3H1 light chain variable region cDNA.
GENESON:T99434	+	21	102	1	Anti-idiotypic antibody 3H1 light chain
GENESON:T30456	+	138	101	1	HNK-20 variable kappa chain coding se
GENESON:Q92503	+	18	100	1	Mouse antibody F4-7 light chain varia
GENESON:T05311	+	0	97	1	MAb SCH94.03 light chain DNA. Monoclo
GENESON:V04640	+	-60	96	1	Mus musculus A17 antibody light chain
GENESON:Q14651	+	30	94	1	R6-5-D6 anti-ICAM-1 light chain. New
GENESON:Q14801	+	30	94	1	Encodes murine anti-ICAM monoclonal a
GENESON:T04625	+	-87	94	1	Mouse derived light chain R73 phage a
GENESON:V63620	+	498	93	1	Nucleic acid sequence of plasmid pET-
GENESON:V63619	+	57	93	1	Nucleic acid sequence of plasmid pET-
GENESON:V63616	+	426	93	1	Nucleic acid sequence of plasmid pET-
GENESON:V63617	+	465	93	1	Nucleic acid sequence of plasmid pET-
GENESON:T94968	+	294	93	1	R. pipiens recombinant Rhase ronc fus
GENESON:T94967	+	-60	93	1	R. pipiens recombinant Rhase ronc fus
GENESON:T94966	+	-60	93	1	R. pipiens recombinant Rhase ronc fus
GENESON:T94965	+	300	93	1	R. pipiens recombinant Rhase ronc fus
GENESON:T94964	+	294	93	1	R. pipiens recombinant Rhase ronc fus
GENESON:T94963	+	366	93	1	R. pipiens recombinant Rhase ronc fus
GENESON:Q90431	+	-60	93	1	R. pipiens recombinant Rhase ronc fus
GENESON:Q15113	+	-12	90	1	DNA encoding anti-idiotypic antibody 1
GENESON:T04625	+	85	85	1	IL-2 chimeric antibody light chain cl
GENESON:N91657	+	-84	85	1	Mouse derived light chain R73 phage a
GENESON:Q85387	+	-63	84	1	Chimeric antibody light chain variabl
GENESON:Q46088	+	31	83	1	MAb 4197X light chain variable region
GENESON:Q30759	+	345	83	1	Sequence encoding 741 sfv-PE40. New s
GENESON:Q08608	+	0	82	1	ME4 light chain V Region (mouse). Chi
GENESON:Q45662	+	60	82	1	Mouse C4G1 Ig light-chain coding sequ
GENESON:Q45662	+	0	82	1	Mouse C4G1 Ig light-chain coding sequ

*Not sequences containing matches at least 15 nt long*

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145	16	8	1	405	11	661066	Anti-cancer monoclonal	4	23e-11
146	16	8	1	411	13	717889	Humanized variable 11	4	23e-11
147	16	8	3	413	13	717890	Humanized variable 12	4	23e-11
148	36	8	3	413	15	737899	Humanized variable 11	4	23e-11
149	36	8	3	417	15	099432	DNA encoding anti-1d1	4	23e-11
150	36	8	3	420	14	196647	DNA sequence encoding	4	23e-11
151	36	8	3	430	15	762537	DNA sequence encoding	4	23e-11
152	36	8	3	432	5	028740	CDNA sequence encoding	4	23e-11
153	36	8	3	445	5	028740	CDNA sequence encoding	4	23e-11
154	36	8	3	459	11	762537	Anti-IL18 heavy chain V	4	23e-11
155	36	8	3	717	29	195310	Murine anti-platelet V	4	23e-11
156	36	8	3	777	30	195310	Anti-IL18 heavy kappa C	4	23e-11
157	36	8	3	777	30	195310	Anti-IL18 heavy kappa C	4	23e-11
158	36	8	3	1657	7	045453	Sequence encoding of L	4	23e-11
159	36	8	3	1657	7	045453	Sequence encoding of L	4	23e-11
160	36	8	3	5300	30	162938	3f1 human IgG4 exons	4	23e-11
161	36	8	3	318	9	046000	Sequence of the variable	3	09e-11
162	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
163	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
164	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
165	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
166	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
167	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
168	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
169	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
170	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
171	35	8	0	318	11	062122	Anti-IL18 heavy chain V	3	09e-11
172	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
173	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
174	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
175	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
176	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
177	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
178	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
179	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
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186	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
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188	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
189	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
190	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11
191	34	7	8	330	37	735544	Anti-IL18 heavy chain V	3	09e-11</

196	31	7.1	46.40	741287	Monoclonal antibody 1	7.2e-11
197	31	7.1	46.34	740810	Primer for amplifying	7.2e-11
198	31	7.1	46.32	740811	Mon kappa chain con	7.2e-11
199	31	7.1	46.7	740812	Mon lambda chain con	7.2e-11
200	31	7.1	55.3	078720	Primer to amplify CM2	7.2e-11
201	31	7.1	819.3	020381	Sequence encoding the	7.2e-11
202	31	6.9	30.11	050503	Anti-cancer monoclonal	4.8e-10
203	31	6.9	30.11	050504	Anti-cancer monoclonal	4.8e-10
204	30	6.9	30.5	018866	Anti-cancer monoclonal	4.8e-10
205	30	6.9	30.5	090399	Light chain primar...	4.8e-10
206	30	6.9	30.21	715156	3H1 V <sub>H</sub> region 3' prim	4.8e-10
207	30	6.9	30.11	067574	Monoclonal antibody KC-4	4.8e-10
208	30	6.9	30.11	067575	Monoclonal antibody KC-4	4.8e-10
209	30	6.9	30.39	028552	Primer-Chappa for mon	4.8e-10
210	30	6.9	30.5	028756	3F9 V <sub>H</sub> -human C-kappa	4.8e-10
211	30	6.9	30.37	700418	Human antibody S6G.1	4.8e-10
212	30	6.9	30.37	700419	Human antibody S6G.1	4.8e-10
213	30	6.9	30.34	765156	Mouse immunoglobulin	4.8e-10
214	30	6.9	30.32	731546	Monoclonal antibody 15	4.8e-10
215	30	6.9	38.9	035439	Sequence reverse comp	4.8e-10
216	30	6.9	38.9	035440	Primer anti-epitopic	4.8e-10
217	30	6.9	54.33	078725	Primer anti-epitopic	4.8e-10
218	30	6.9	68.17	029025	Murked complementari	4.8e-10
219	30	6.9	66.35	737063	Mutant CDR oligonucle	4.8e-10
220	30	6.9	188.14	089314	S4134 VX-1 gene	4.8e-10
221	30	6.9	188.14	089315	S4134 VX-1 gene	4.8e-10
222	30	6.9	321.37	768403	CDN for anti-TNF- $\alpha$ p	4.8e-10
223	30	6.9	321.34	766761	Anti-cancer specific	4.8e-10
224	30	6.9	312.29	761236	Human anti-RSV monoc	4.8e-10
225	30	6.9	312.29	761235	Anti-LTR-beta antibo	4.8e-10
226	30	6.9	312.29	761234	Anti-LTR-beta antibo	4.8e-10
227	30	6.9	33.9	055917	Humanized light chain	4.8e-10
228	30	6.9	369.16	090434	DNA encoding anti-Id1	4.8e-10
229	30	6.9	369.16	090435	DNA encoding anti-Id1	4.8e-10
230	30	6.9	369.16	090436	DNA encoding anti-Id1	4.8e-10
231	30	6.9	389.14	067194	Humanized light chain V	4.8e-10
232	30	6.9	389.17	715181	HL108 V <sub>H</sub> encoding as	4.8e-10
233	30	6.9	429.2	011055	Sequence encoding 11g	4.8e-10
234	30	6.9	429.2	011056	Sequence encoding 11g	4.8e-10
235	30	6.9	723.92	021098	pacr- $\alpha$ 01 encoding an	4.8e-10
236	30	6.9	747.3	021098	DNA encoding human s	4.8e-10
237	30	6.9	1553.9	051229	Vector coding XMG-9	4.8e-10
238	30	6.9	9106.11	053535	Light chain variable	4.8e-10
239	30	6.7	321.15	091508	Light chain variable	3.2e-09
240	29	6.7	324.11	064060	Anti-cancer monoclonal	3.2e-09
241	29	6.7	324.11	064060	Anti-Pseudomonas aeru	3.2e-09
242	29	6.7	324.11	064060	Anti-Pseudomonas aeru	3.2e-09
243	29	6.7	422.16	098848	Anti-Pseudomonas antio	3.2e-09
244	29	6.7	422.16	098848	Anti-Pseudomonas antio	3.2e-09
245	29	6.7	7051.37	769310	Single chain anti-Id4	3.2e-09
246	29	6.7	1061.38	791971	R. pliptans recombinan	3.2e-09

217	106	6	7	106	8	44933	Human anti-IL-8 light
218	106	6	7	106	8	44934	Human anti-IL-8 heavy
219	117	3	3	117	3	90317	Single chain anti-IL-8
220	117	3	3	117	3	90318	Single chain anti-IL-8
221	37	18	6	37	18	700432	Murine IL-8 (5.11.14)
222	37	18	6	37	18	700355	Anti-IL-8 (5.11.14)
223	37	18	6	37	18	700355	Monoclonal antibody 5
224	37	18	6	37	18	700355	Monoclonal antibody 5
225	37	18	6	37	18	700355	Monoclonal antibody 5
226	37	18	6	37	18	700355	Monoclonal antibody 5
227	37	18	6	37	18	700355	Monoclonal antibody 5
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234	37	18	6	37	18	700355	Monoclonal antibody 5
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271	37	18	6	37	18	700355	Monoclonal antibody 5
272	37	18	6	37	18	700355	Monoclonal antibody 5
273	37	18	6	37	18	700355	Monoclonal antibody 5
274	37	18	6	37	18	700355	Monoclonal antibody 5
275	37	18</					

[illegible]



553	19	4	4	342	6	Q33032	Mb GH variable seq	1	136	0
554	19	4	4				Monoclonal antibody G	1	136	0
555	19	4	4				Anti-MGF beta-1-seq	1	136	0
556	19	4	4	347	34	T60383	Human monoclonal anti	1	136	0
557	19	4	4	351	20	T18634	Human monoclonal anti	1	136	0
558	19	4	4	352	20	T12128	Human monoclonal anti	1	136	0
559	19	4	4	359	21	T72930	Monoclonal antibody L	1	136	0
560	19	4	4	361	21	T12930	Switched VL region Ka	1	136	0
561	19	4	4	372	10	Q50567	Human IL-1 chimeric a	1	136	0
562	19	4	4	381	5	Q30759	Human IL-1 light chain	1	136	0
563	19	4	4	381	7	Q45662	Mouse Ccgl Ig light-c	1	136	0
564	19	4	4	382	34	T73511	CDNA encoding light c	1	136	0
565	19	4	4	391	16	Q50511	Human anti-CD3 light c	1	136	0
566	19	4	4	393	16	T05214	Humanized antibody Jb	1	136	0
567	19	4	4	393	14	Q33866	Humanized antibody Jb	1	136	0
568	19	4	4	393	14	Q33830	Encodes V region of L	1	136	0
569	19	4	4	400	7	Q40429	Humanized antibody Jb	1	136	0
570	19	4	4	400	7	T73824	Humanized antibody Jb	1	136	0
571	19	4	4	410	29	T73824	Light chain transmem	1	136	0
572	19	4	4	444	25	Q30830	MB N4 light chain v	1	136	0
573	19	4	4	444	25	Q30830	MB4 Light Chain v Reg	1	136	0
574	19	4	4	444	25	Q30830	Regn light chain trans	1	136	0
575	19	4	4	470	36	T31590	Light chain transmem	1	136	0
576	19	4	4	470	29	T32820	Light chain transmem	1	136	0
577	19	4	4	484	34	T90021	DNA encoding light ch	1	136	0
578	19	4	4	554	34	Q50221	Encodes V region of L	1	136	0
579	19	4	4	723	7	Q42288	Human anti-CD3 light c	1	136	0
580	19	4	4	723	7	Q42288	V-1(gamma)(L)/L58T	1	136	0
581	19	4	4	729	38	V06147	Chimeric monoclonal a	1	136	0
582	19	4	4	729	40	V01616	Chimeric MAb 6G4 2.5	1	136	0
583	19	4	4	729	40	V01616	Chimeric monoclonal a	1	136	0
584	19	4	4	729	33	T78394	Chimeric monoclonal a	1	136	0
585	19	4	4	729	38	V03266	Human variable regio	1	136	0
586	19	4	4	729	17	T03380	Anti-L18-chimeric 6G	1	136	0
587	19	4	4	748	14	T02882	ScpE(PW51) CDNA.	1	136	0
588	19	4	4	748	14	T02882	Encodes V kappa region	1	136	0
589	19	4	4	768	6	Q45442	Encodes V kappa region	1	136	0
590	19	4	4	809	10	Q56734	Sequence of single ch	1	136	0
591	19	4	4	812	9	V72110	Human DNA fragment Vx	1	136	0
592	19	4	4	812	9	V72110	Human DNA fragment Vx	1	136	0
593	19	4	4	812	11	Q78852	Human V kappa-seg Vx	1	136	0
594	19	4	4	812	7	T78780	DNA fragment Vx5.3, k	1	136	0
595	19	4	4	866	7	Q45504	Sequence of single ch	1	136	0
596	19	4	4	866	7	Q45504	Sequence of single ch	1	136	0
597	19	4	4	900	78	T73161	DNA fragment Vx6.5, k	1	136	0
598	19	4	4	900	78	Q47231	Human DNA fragment Vx	1	136	0
599	19	4	4	900	78	Q47231	Human DNA fragment Vx	1	136	0
600	19	4	4	900	12	Q78852	Human DNA fragment Vx	1	136	0
601	19	4	4	934	10	Q18187	Specific anti-CD-56/93	1	136	0
602	19	4	4	1028	7	Q45068	Sequence of polydip	1	136	0
603	19	4	4				Sequence of polydip	1	136	0
19				1031	36	T91858	Growth factor THER DN	1	136	0

[illegible]

655	18	4.1	342.11	Q74304	Humaneled DRP1, light	6.50e-02
654	18	4.1	372.39	Q71799	Humaneled anti-CEA an	6.50e-02
653	18	4.1	376.11	Q75915	Receptor human Rgpap	6.50e-02
652	18	4.1	376.11	Q75915	Anti-human IL-6 chain	6.50e-02
651	18	4.1	376.11	Q75914	PBL3/Humaneled light	6.50e-02
650	18	4.1	378.9	Q71553	Humaneled light	6.50e-02
649	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
648	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
647	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
646	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
645	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
644	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
643	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
642	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
641	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
640	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
639	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
638	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
637	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
636	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
635	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
634	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
633	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
632	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
631	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
630	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
629	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
628	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
627	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
626	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
625	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
624	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
623	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
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617	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
616	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
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609	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
608	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
607	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
606	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
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603	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
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599	18	4.1	378.9	Q71552	Humaneled light	6.50e-02
598	18	4.1</				

706	18	506	5	031362	ROC-RN5-PNA	6.60e-01
707	18	527	1	021462	Anti-CD151	6.60e-01
708	18	530	14	072226	Human rephed NM	6.60e-01
709	18	608	1	090500	Light chain antibody	6.60e-01
710	18	616	1	189463	Sequence of human	6.60e-01
711	18	619	1	095050	Genomic sequence of	6.60e-01
712	18	632	10	065001	Sequence encoding	6.60e-01
713	18	632	10	043773	Sequence encoding	6.60e-01
714	18	702	7	043773	Human antibody 80	6.60e-01
715	18	705	39	012297	Humanized heavy chain	6.60e-01
716	18	715	1	013155	Anti-trasferrin D701	6.60e-01
717	18	746	24	025565	Rephed CD4 antibody	6.60e-01
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719	18	748	4	025565	Rephed CD4 antibody	6.60e-01
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742	18	748	4	025565	Rephed CD4 antibody	6.60e-01
743	18	748	4	025565	Rephed CD4 antibody	6.60e-01
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747	18	748	4	025565	Rephed CD4 antibody	6.60e-01
748	18	748	4	025565	Rephed CD4 antibody	6.60e-01
749	18	748	4	025565	Rephed CD4 antibody	6.60e-01
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765	18	748	4	025565	Rephed CD4 antibody	6.60e-01





[illegible]

FT		/cseg= b
PR	107101959-8.	
D6	-NMR 1993.	
PD	16 -NMR 1993.	272850.
PR	06-OCT-1993; JP-	272950.
PA	(BACU.) HAOJIMAYA T.	
DR	WPI: 55-182897/24.	
PT	Bovine anti-idiotypic antibody against an animal antiserum monoclonal	
PT	antibody - and DNA sequences encoding the antibody, useful in	
PT	pharmacology, medicine and biochemical fields.	
CC	GENSEI, 500-1495 1pp; Jpnpt; Japanese	
CC	Idiot(1) Idiot(2) Idiot(3)	
CC	monoclonal antibody Three antibodies and DNA encoding them are useful	
CC	In Pharmacological, medical and biochemical fields of research.	
SC	Sequence 438 BP; 104 M; 110 C;	112 G; 102 T;
Qy	Query Match 20.7%; Pred No: 0; DB 16;	Length 438;
	Beat Local Similarity 90.0; Gapd No: 138r-65;	
	Matches 0; Conservative 0;	Mismatches 0; Indels 0; Gaps 0.
D6	334 tcaaccctgcggcgaggagacgaacgagaaataaacggcgatccgttcacatttca 393	
Qy	346 TCACCCTGCAGGCGGGCAGCAACGCCATGTAAACACGGCATTCCTCACACTGA 405	
D6	394 tcaactttcccctcaccttcgccagttaatttg 423	
Qy	406 TCAAATTCCCACACATCCACGTAACACTTGGC 435	
RESULT:		
S		
ID	785091 standard: cDNA; 642 BP.	
CD	1580bp; 1997.	
D2	House monoclonal antibody B9 light chain encoding cDNA.	
NM	Human plasma apolipoprotein B-100; arterioletherosclerotic lipoproteins;	
KV	antibody; Fab; de.	
FR	Key medicinal.	
PH	Location/Qualifiers	
CDS	1..642	
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FT	/product= B9L	
FT	/note= Stop codon not shown*	
FT	mlec.feature	
FT	322..642	
FT	/cseg= b	
FT	/label= Chappa	
PD	J09315487-7.	
PD	17-JUN-1997.	
PD	09-MAY-1996;	114492.
PR	02-NOV-1995; KR-	Oj39459.

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PA      (KAO) JOSEPH SCI & TECHNOLOGY RES CENT.
PR      WPI: 97-567087/34.
PN      Deposition Date: 07/20/98.
PT      B-100 - useful for removing atherosclerotic lipoprotein(s).
PS      Claim 4; Fig 6; 11pp; Japanese.
PC      The present sequence encodes the mouse monoclonal antibody 9S 11gE
CC      C-100. The nucleic acid can be used in a method for immunization
CC      of a recombinant antibody which specifically binds human plasma
CC      apolipoprotein B-100. The antibody can be used as a reagent for
CC      determining the concentration of human plasma apoB/aprotein B-100
CC      selectively removing athero-electrostatic lipoproteins containing human
CC      plasma apolipoprotein B-100.
SQ      Sequence   642 BP:    188 A;    152 C;    152 G;    150 T;

Query Match          15 5%; Score 65; DB 13; Length 642;
Beat Local Similarity 100.0%; Pstd No. 1, 02e-60;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Dh       282 tgcctcagcggttcggataggacgaaccacccgatataaacagcgcatatgacctcaacac 341
Db        342 tccttccacgcccttgacaagggcggcccacaaactgtaattaaaacggcgtatccgcacnccac 401
Oy         342                                     :                               :
           342 ttttttcccccttcctccacacccccctc 366
Oy        402 ttatccatcttccacacccccctccagt 426

RESULT:             { 4 }
ID            6 standard; DMW: 652 kDa;
AC            TGTTGATL     972 f(fate antigen)
DE            Antibody 352 light chain variable region coding sequence.
RW            catalytic activity: enantiomericselective hydrolases; hydrolidma;
RM            ZAAWGJ; ZAAAGG; da.
NM            NIA.
OS            Mus.
PE            cd3
PF            /cd3
FT            Location/multipliers
F1              1 651
F2              /+tag=
F3              /product= antibody 7612 light chain variable region
F4              protein analysis: nonmeme codon TAA exists at
F5              positions 619-645
F6
F7
F8
F9

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DR	P-280D 15395.	Catalytic antibody for enantioselective hydrolysis of amino acid ester.
PR	Also new hydrolase secreting the antibody	
PC	Present disclosure new class of antibodies which hydrolyse amino acid ester enantioselectively. Preferably the esters are 4-nitro-benzyl ester and the esterified amino acids are amino-protected.	
CC	Also disclosed are new hydrolases expressing the catalytic antibodies, and the antibodies are related to those using the compound p-nitrobenzyl 4-carboxy-L-(benzylloxycarbonylamino)-butyl-L-pipeconyl.	
CC	They are used for efficient resolution of racemic amino acids with	
CC	for the production of optically active drugs and chiral separation agents.	
CC	The present sequence represents the coding sequence for the	
CC	variable region of the light chain of antibody 502, produced by	
CC	sequence 652 DP.	
CC	Sequence 652 DP: 194 A: 151 C: 154 G: 153 T:	
CC	Query Match: 15 58: Score 85: DB 31: Length 652:	
CC	Matches 85: Conservative: 0 Mismatch: 0 Indels 0: Gaps 0	
DB	282 tccatccacgtctctggaagggggacacgaacgaagaataaaggagcagatgagaccacac 341	
CC	342 acgcac 401	
DB	342 tttatccatctctccac 366	
CC	402 tccac 426	
CC	RESULTS	
AC	092803 standard: cDNA, 723 BP.	
AC	092803:	
DB	07-EB9 1996 (flat entry)	
DB	Mouse antibody P-7 light chain variable region coding sequence.	
CC	Primer amplification CC: mouse: kappa chain: heavy chain: Fab:	
CC	variable region: antigen: immunoreactive: cell surface marker: foetal:	
CC	cancer: stem cell: metastasis: therapy: Alzheimer's disease: hydrolase:	
CC	famial: hypercholesterolemia: binding affinity: ds.	
CC	Key words:	
CC	Location/Qualifiers	
CC	61..359	
CC	/tag a	
CC	/product- antibody P-7 light chain variable region	
CC	W09515082.A2	
CC	15-JUN-1995.	
CC	08-DEC-1994: 014106.	







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P1 5a11-precursor chlamic polypeptide comprising biologically active
P2 sequence and single-chain antibody sequence - has resistance to e.g.
P3 3.
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PR 21 JDN-1988: US-205748.
PR 21 AOC-1982: US-938505.
PR 21 AOC-1982: US-938505.
PA (HRR): HRR1285 UNL.
P1 Ramjeeasingh M, Rochnett A, Shami Et.
WP1: 97-558400/31.
DR 21 JDN-1988: US-205748.
CC The present sequence is a chimeric polypeptide comprising biologically active
CC sequence and a chimeric polypeptide containing a proteolytic enzyme, e.g.
CC P7 displaying temperature presence of proteolytic enzymes, etc.
CC Example 3, Column 27-30, 29pp. English.
CC The present sequence is a chimeric gene containing the cDNA for
CC a murine anti-aparaginsin II monoclonal chain variable regions of a
CC aparaginsin II. The gene was used in the preparation of a novel
CC recombinant chimeric polypeptide, comprising a 1st region
CC containing an antigenically active domain and another domain
CC including a single chain antibody (SCA) having the 1st region
CC chain of an antibody variable region which specifically binds the
CC complement of the 1st region. The chimeric polypeptide assumes a
CC conformation that is biologically active. The epitope of the 1st
CC region and protects for biological activity. The polypeptide
CC denaturing temperature or pH conditions, proteolytic enzymes, or
CC oxidizing agents or alcohol. The regions of the chimeric
CC antibody-chain complex form a structure analogous to an
CC the above type has better tryptic resistance than free
CC sequence. 1888 BP: 435 A: 498 C: 517 G: 398 T:
DQ
DQ Query March 16, 1991: Score: 70. DB 37: Length 1088:
DQ Best Local Similarity 100.0%: Pident. No. 288e-46:
DQ Matched 70: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DQ 293 CAGCTCGTGGAGGAGACCAACGTGGATATGATACAGCGCTATGATGCGCAATGATGATC 350
DQ |||||||
DQ 348 CAGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 407
DQ |||||||
DQ 408 CAGCTCGCA 417
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DQ 351 CAGCTCGCA 360
DQ |||||||
DQ 408 CAGCTCGCA 417
DQ
DQ RESULT 17
DQ ID T04625 standard: DMA: 270 BP.
DQ DC 2704625: 1986 (1st seq)
DQ DE Mouse derived light chain R33 phage antibody pattern A DMA.
DQ FM Light chain: R33: murine: catalytic antibody, bacteriophage.
DQ pattern A: ss.

```

PH	Key	Location/Qualifiers
PT	cds	1..270
FF	/tag	"A"
FT	/note	"partial peptide"
PV	M09527045.n1.	
PR	13-OCT-1995.	
PR	30-MAR-1994.	0036280
PA	(ICGN.) ICGN INC.	0036280.
E1	Chiswell H., Darvelay M.J., Fitzgerald K., Kenten J.B., Martin M.T., McCormick E.V., Smith R.C., Williams N.D.	
D1	P-PDB: 880078.	
PT	Production of catalytic libraries displayed on phage - by generating a gene library of antibody-derived domains and expressing them in phage vectors [http://English.biology.duke.edu/~chris/papers/antibody.htm]	
CC	The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CA can be used to activate/deactivate A or formation of ion in an assay by enhancing the rate of cleavage.	
SO	Sequence 270 BP; 65% A; 62 C;in 63 G; 75 T;	
<hr/>		
Query Match	Similarity: 13.9%; Score 65; DB 17; Length 270;	
Matches	95; Conservative: 0; Identical: 139; A1:	
OY	184 GCACATTCAGGACGGCAGGCATGACGCCCATCCGCTTTGGTCTCCGAGGATCCCAAAAGG 156	
Db	157 TTCGATTGGCACTTAGTGCTCGAGGTGCATCTTATCCATCC 193	
OY	244 TTCCGCGCACATTAAGCTGCTGCGGCTGCGGATTCATATCTCTCA 280	
<hr/>		
RESULT	18 standard: cDNA: 739 BP.	
AC	T1888D.	
DT	29-OCT-1996 (first entry)	
DE	S20C5 anti-c-erbB-2 two single chain Fv construct.	
KM	S20C5 anti-c-erbB-2 monoclonal antibody; single chain Fv; afv;	
KW	in vivo immunization of mice; linker: C-terminal amino acid sequence;	
RV	increased binding avidity; tissue retention time; ss.	
PS	monom. sepiens.	
PT	cds	Location/Qualifiers
FF	1..113	
FT	/tag	"A"
FT	/note	"START codon absent"

```

PR 005314254.A.
PR 06-PED-1992. 8131667.
PR 06-PED-1992. US-831667.
PR 07-OCY-1993. US-831804.
PR 08-OCY-1993. US-831804.
PA (CERN). CERN/SCB B1000/SCB1005 INC
P1 Houston Liv. Resour. Jts. Oppemann R. Ring DB:
DR WPI. 96-333164/33.
PT Compn: W02020.
PT Compn: W02020.
PS comprising dimer of single-chain Fv fragments
PS Example 1: Columns 31-36; 30bp. Light
PS Example 2: Columns 37-42; 30bp. Heavy
PS A 1500-bp heavy (VH) and variable light (VL) genes were cloned from
CC a 1500-bp heavy (VH) and variable light (VL) genes were cloned from
CC antibody constant and joining regions. The VH and VL genes with a (SPV)
CC gene was constructed by connecting the VH and VL genes with a (SPV)
CC Ser rich polypeptide linker. The resulting 5200's two SPV gene, the
CC transformed into E. coli. The resulting 5200's two SPV gene, the
CC admn. of IPV to the culture medium.
CC A compn. comprising a carrier and the 2 SPV protein prod. can be
CC 2 SPV protein. The resulting 5200's two SPV protein prod. can be
CC the same antigen, therefore giving greater binding specificity target
CC longer tissue retention times, compared to individual SPV protein
S0 Sequence 159 bp. 168 A. 177 C. 181 G. 193 T.

Query Match 14.5% Score 63: DB 22: Length 739:
Match Local 98.4% Pct. No. 1,324-39:
Matrix 135: Conservative 0: Mismatch 2: Indels 0: Gaps 0

Db 502 TGGCTCGAGGAGGACCAAGACGACATCATCAATCGCGATCTGACCAATCAGGATTA 561
Gy 163 TGGCTCGAGGAGGACCAAGACATCATCAATCAATCAATCAATCAATCAATCAATCAAT 722
Db 562 GATCGTCGGTCGTCGCAAGGATCGTCGAGCGATCGTCGTCGTCGTCGTCGTCGTCGTCGTC 621
Gy 213 GATCGTCGGTCGTCGCAAGGATCGTCGAGCGATCGTCGTCGTCGTCGTCGTCGTCGTC 622
Db 233 GATCGTCGGTCGTCGCAAGGATCGTCGAGCGATCGTCGTCGTCGTCGTCGTCGTCGTC 622
Gy 233 GATCGTCGGTCGTCGCAAGGATCGTCGAGCGATCGTCGTCGTCGTCGTCGTCGTCGTC 622
Db 632 ATCAG 636
Gy 283 ATCAG 287

RESULT 19
AD 046004 standard: CDNA. 739 bp.
DE 07-PED-1994 (43rat alyp)
DE Sequence encoding 5200's alyp protein.

```









PT US566070-A. to a Lys residue  
PD 11-NOV-1997.  
PI 01-MAR-1995: 398613.  
PR 01-MAR-1995: US-398612.  
PR 01-MAR-1995: US-398614.  
PA (GENT) GENENTECH INC.  
PA (INDV) UNIV INDIANA.  
PI Doerschuk CM, Fong S, Robert CA, Kim KJ, Leong SR;  
P-PSDB: M40124.  
PT Immunotherapy of ulcerative colitis - with monoclonal antibody  
PT Treatment of bacterial pneumonia - with monoclonal antibody specific  
PT for interleukin-8; inhibits lung inflammatory conditions  
PS Example 1: A murine monoclonal antibody (Mab) 6G4.2.5 encoding the region of  
CC anti-rabbit interleukin-8 (IL-8) antibody. IL-8 is a neutrophil  
CC chemotactic peptide secreted by a variety of cells in response to  
CC inflammatory mediators. IL-8 can play an important role in the  
CC defense syndrome (ARDS). septic shock and multiple organ failure.  
CC Treatment of bacterial pneumonia in a mammal comprises administering an  
CC anti-IL-8 monoclonal antibody that binds human IL-8 with a Kd of 8,  
CC inhibits IL-8 mediated neutrophil chemotaxis in response to IL-8,  
CC binds to C5a, beta-7c or platelet factor 4. IL-8 specific monoclonal  
CC antibodies are especially useful for treating pneumonia caused by Streptococcus  
CC pneumoniae, E. coli or Pseudomonas aeruginosa in humans. The antibodies  
CC are used in the treatment of ulcerative colitis and other  
CC inflammatory conditions.  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 39; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 334 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
RESULT 36  
AC 03-JUN-1998 (first entry)  
AD V10310.  
DE Murine monoclonal antibody 6G4.2.5 light chain variable region CDM.  
KW Monoclonal antibody; Mab 6G4.2.5; Interleukin-8; IL-8; murine;  
KW treatment: light chain; heavy chain; neutrophil chemotaxis inhibitors; aa.  
OS Msa sp.  
PH Key Location/Qualifiers  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 37; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 334 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426

PI Doerschuk CM, Fong S, Herbert CA, Kim KJ, Leong SR;  
P-PSDB: M86321.  
PT Inflammatory disorders, partic. ulcerative colitis, and bacterial  
PT Example 2: Fig 24: 114pp: English.  
CC A CDNA insert (703378) in vector pChimFAB codes for the light  
CC chain variable region and part of the constant region of anti-rabbit  
CC interleukin-8 mouse monoclonal antibody 6G4.2.5. The CDNA was cloned  
CC into a pCMV vector (703372) and expressed in COS cells. It is  
CC used with primers (703371-74) based on light chain sequences. It is  
CC in the prodn. of anti-IL-8 mouse-human chimeric Fab.  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 37; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 334 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
RESULT 38  
ID 778588 standard: CDNA: 391 BP.  
AC 03-JUN-1998 (first entry)  
AD V10310.  
DE Murine monoclonal antibody 6G4.2.5 variable light chain region encoding CDM.  
KW Interleukin-8; IL-8; antineoplastic; anti-interleukin-8 antibody; asthma;  
KW inflammatory disorder; neutrophil chemotaxis; elastase release;  
KW ischemic reperfusion; ARDS; dermatitis; bacterial pneumonia;  
KW Msa sp.  
PH Key Location/Qualifiers  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 37; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 334 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426

PT CDS 1,391  
PT /tag- a  
PT /product- 6G4.2.5 light chain variable region  
PD 03-JUN-1998.  
PI 01-MAR-1995: 398613.  
PR 01-MAR-1995: US-398612.  
PR 01-MAR-1995: US-398614.  
PA (GENT) GENENTECH INC.  
PA (INDV) UNIV INDIANA.  
PI Doerschuk CM, Fong S, Robert CA, Kim KJ, Leong SR;  
P-PSDB: M40124.  
PT Immunotherapy of ulcerative colitis - with monoclonal antibody  
PT specific for interleukin-8  
PS Example 1: A murine monoclonal antibody (Mab) 6G4.2.5 encoding the region of  
CC anti-rabbit interleukin-8 (IL-8) antibody. IL-8 is a neutrophil  
CC chemotactic peptide secreted by a variety of cells in response to  
CC inflammatory mediators. IL-8 can play an important role in the  
CC defense syndrome (ARDS). septic shock and multiple organ failure.  
CC Treatment of bacterial pneumonia in a mammal comprises administering an  
CC anti-IL-8 monoclonal antibody that binds human IL-8 with a Kd of 8,  
CC inhibits IL-8 mediated neutrophil chemotaxis in response to IL-8,  
CC binds to C5a, beta-7c or platelet factor 4. The anti-IL-8 antibodies can also be used  
CC for the treatment of bacterial pneumonia. 94 G: 97 T:  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 39; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 334 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
RESULT 37  
ID 703378 standard: CDNA: 391 BP.  
AC 03-JUN-1998 (first entry)  
AD V10310.  
DE Anti-IL-8 Mab 6G4.2.5 light chain variable region CDM.  
KW Monoclonal antibody; Mab 6G4.2.5; Interleukin-8; IL-8;  
KW chimeric antibody; Fab; antibody engineering; inflammation;  
KW inflammatory bowel disease; ulcerative colitis; bacterial pneumonia;  
KW Msa sp.  
PH Key Location/Qualifiers  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 37; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 334 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426

CC Methods for treating asthma in mammals with interleukin-8 (IL-8)  
CC monoclonal antibody. The present invention provides a CDNA 6G4.2.5  
CC monoclonal antibody is an anti-IL-8 antibody. The present sequence  
CC encodes the variable light chain region of murine 6G4.2.5 monoclonal  
CC antibody. Anti-IL-8 antibodies are especially used to treat or prevent  
CC asthma in mammals. The antibodies are also used to treat or prevent  
CC response to IL-8 (B) IL-8-mediated release of neutrophil chemotaxis  
CC and (C) binding of IL-8 to neutrophils. Anti-IL-8 antibodies can be used  
CC to treat many other inflammatory disorders, e.g. ischemic reperfusion,  
CC ARDS, dermatitis, particularly bacterial pneumonia and inflammatory  
CC diseases.  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 37; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426  
RESULT 39  
ID 793517 standard: CDNA: 391 BP.  
AC 03-JUN-1998 (first entry)  
AD V10310.  
DE Murine Mab (6G4.2.5) light chain variable region encoding CDM.  
KW murine light chain; 6G4.2.5; human interleukin-8; IL-8; anti-IL-8;  
KW monoclonal antibody; Mab; diagnosis; inflammatory disorder; treatment;  
KW constant region; chimeric; neutrophil chemotaxis; aa.  
KW Msa sp.  
PH Key Location/Qualifiers  
SQ Sequence 391 BP: 95 A: 105 C: 94 G: 97 T:  
Query Match 11.0%; Score 48; DB 37; Length 391;  
Best Local Similarity 100.0%; Pred. No. 9,846-76;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 379 AACGGGCTGATGCTGCACACATGTCATCTCCACATCCAGT 426









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check: 7546 from:

FROMIG of: /home/obryen/ree455/olig/US08836455.seq  
sequence 1, application us/08836455

general information:

applicant: chatterjee, malaya  
applicant: foon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: GenBank: \* Sequences: 602,539 Total-length: 1,199,477,030 April 18, 1999 18:59

#### Database Release Information:

GenBank, Release 110.0, Released on 14Dec1998, Formatted on 15Dec1998  
EMBL, Release 56.0, Released on 15Sep1998, Formatted on 15Dec1998

Word-size: 15 Words: 182747 Diagonals: 6,088 Total diagonals: 2,000,000,000  
Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 116.94

Sequence Stord Diag Score Width Documentation ..

GB_RO:MSIRKCC	+	5	332	1	141880 Mus musculus immunoglobulin ka
GB_PAT:AR007981	+	339	306	1	AR007981 Sequence 5 from patent US 57
GB_PAT:123446	+	339	306	1	123446 Sequence 5 from patent US 5534
GB_RO:AF045508	+	0	305	1	AF045508 Mus musculus dc10 anti-poly
GB_RO:MSUX	+	-60	304	1	L48667 Mus musculus (cell line C3H/F2
GB_RO:AF045510	+	0	298	1	AF045510 Mus musculus 6C9 monoclonal
GB_RO:AF045495	+	0	294	1	AF045495 Mus musculus dc4 anti-poly
GB_RO:MMU55591	+	-68	291	1	U55591 Mus musculus anti-DNA immunog
GB_RO:MSIGKAC1	+	252	284	1	U00565 Mouse Ig kappa active gene: VK
GB_RO:MMIGK7	+	253	284	1	V00808 Part of the murine gene for ka
GB_RO:MMU55588	+	-69	281	1	U55588 Mus musculus anti-DNA immunog
GB_RO:MSIGLAF4	+	-78	280	1	M36246 Mouse Ig kappa-chain mRNA V re
GB_RO:AF003293	+	225	273	1	AF003293 Mus musculus Ig kappa light
GB_RO:MSIGKVC	+	253	273	1	V00566 Mouse Ig kappa germline V gene
GB_RO:MMIGK3	+	253	273	1	V00804 Murine kappa-immunoglobulin ge
GB_PAT:107835	+	-75	273	1	M64168 Mus musculus Ig active kappa-c
GB_PAT:107835	+	-60	271	1	107835 Sequence 4 from patent EP 0088
GB_PAT:103643	+	-60	271	1	103643 Sequence 4 from patent US 4642
GB_RO:MMU29617	+	-60	270	1	U29617 Mus musculus anti-DNA antibody
GB_RO:MSIGKAA3	+	-63	268	1	M59920 Mouse Ig germline chain mRNA V
GB_RO:MMU8675	+	42	265	1	U88675 Mus musculus anti-DNA antibody
GB_RO:MMVKMRB11	+	-60	265	1	X63811 M.musculus mRNA for IgM V(K)MR
GB_RO:MMIGGVJ1	+	-19	249	1	X02177 M.musculus mRNA for IgG kappa
GB_RO:MMU30236	+	-60	245	1	U30236 Mus musculus anti-DNA antibody
GB_RO:MMU8676	+	-75	241	1	U88676 Mus musculus anti-DNA antibody
GB_RO:MDIGKVB5	+	-60	241	1	Z22118 M.domesticus Igk variable regi
GB_RO:MSIGKCA	+	-10	233	1	M12191 Mouse Ig active kappa-chain VJ
GB_RO:MMIGG1VL	+	-60	232	1	X82890 M.musculus Iggl, light chain V
GB_RO:MMU25098	+	-60	230	1	U25098 Mus musculus anti-Pseudomonas
GB_RO:SS6053	+	-80	230	1	S69053 Ig V kappa -anti-P-nitrophenyl
GB_RO:AF003294	+	218	229	1	AF003294 Mus musculus Ig kappa light
GB_RO:MMIGGVJ2	+	-18	226	1	X02178 M.musculus mRNA for IgG kappa
GB_RO:MMU62776	+	-60	212	1	U62776 Mus musculus immunoglobulin l
GB_RO:MMU19320	+	-84	210	1	U19320 Mus musculus immunoglobulin ka
GB_RO:AF003291	+	-60	206	1	AF003291 Mus musculus IgG kappa light
GB_RO:AF003299	+	-60	203	1	AF003299 Mus musculus IgG kappa light
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GB_RO:MSIGKAE	+	486	190	2	U00568 mouse Ig kappa unproductively
GB_RO:MMIG04	+	486	190	2	V00760 Mouse pseudogene for kappa-imm
GB_RO:AB016620	+	10	182	1	AB016620 Mus musculus mRNA for Immun
GB_RO:MMIGKCA1	+	-78	182	1	X03382 Mouse mRNA for GAT (HP27) anti
GB_RO:MMALCVR27	+	-60	180	1	X90902 M.musculus antibody light chain
GB_RO:AF003300	+	-60	178	1	AF003300 Mus musculus IgG kappa light
GB_RO:SS5170	+	-57	178	1	SS5170 nitrophenyl phosphate-specif
GB_RO:MMU19327	+	-114	175	1	U19327 Mus musculus immunoglobulin ka
GB_RO:MMIGKGA2	+	-84	174	1	X03383 Mouse mRNA for GAT (HP22) anti
GB_RO:MMIGKGA3	+	-105	162	1	X03384 Mouse mRNA for GAT (HP29) anti
GB_RO:MMU19326	+	-126	156	1	U19326 Mus musculus immunoglobulin ka

*# of sequences containing matches at least 15 nucleotides long*

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[illegible]

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Dh	223	GGTGTGCTATGCTCCCAAAAGGCTATGCTATGCTGCTATGCTATGCTATGCTATGCT	282		
Dh	223	ATACGACGCTATATATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT	282		
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Dh	343	CCGT 346			
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DEFINITION	Sequence 4 from Patent EP 0088994.				
ACCESSION	U0088994				
KEYWORDS	g889447				
ORIGIN	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 324)				
AUTHORS	Moore, K.W. and Effraim, A.				
TITLE	Hybrid DNA binding composition prepared thereby and processes				
JOURNAL	Patent: EP 0088994-2 & 21-sep-1983.				
FEATURES	Location/Qualifiers				
source	1..324	/org="Unknown"			
BASE COUNT	82 a	80 c	75 g	87 t	
ORIGIN					
Query Match	28.0%	Score 127	DB 221	Length 324:	
Best Local Similarity 98.9%		Pred. No. 6.0e-112:			
Matches 1827	Conservative	0	Mismatches 2	Indels 0	Gaps 0
Dh	103	TCGCTTACGACGACACACAGATATATTAACGCTATATACGACACACACATTA	163		
Dh	163	TGGCTTACGACGACACACAGATATATTAACGCTATATACGACACACACATTA	222		
Dh	163	ATCGATGCTATGCTCCCAAAAGGCTATGCTATGCTGCTATGCTATGCTATGCTATGCT	222		
Dh	223	GGTGTGCTATGCTCCCAAAAGGCTATGCTATGCTGCTATGCTATGCTATGCTATGCT	282		
Dh	223	ATACGACGCTATATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT	282		
Dh	283	ATACGACGCTATATGATATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCT	342		
Dh	283	CCGT 286			
Dh	343	CCGT 346			
LOCUS	107835	324 bp		PAT	14-NOV-1994
DEFINITION	Sequence 4 from Patent EP 0088994.				
ACCESSION	U0088994				
KEYWORDS	g889447				
ORIGIN	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 324)				
AUTHORS	Moore, K.W. and Effraim, A.				
TITLE	Hybrid DNA binding composition prepared thereby and processes				
JOURNAL	Patent: EP 0088994-2 & 21-sep-1983.				
FEATURES	Location/Qualifiers				
source	1..324	/org="Unknown"			
BASE COUNT	82 a	80 c	75 g	87 t	
ORIGIN					
Query Match	28.0%	Score 127	DB 221	Length 324:	
Best Local Similarity 98.9%		Pred. No. 6.0e-112:			
Matches 1827	Conservative	0	Mismatches 2	Indels 0	Gaps 0
Dh	103	TCGCTTACGACGACACACAGATATATTAACGCTATATACGACACACACATTA	163		
Dh	163	TGGCTTACGACGACACACAGATATATTAACGCTATATACGACACACACATTA	222		
Dh	163	ATCGATGCTATGCTCCCAAAAGGCTATGCTATGCTGCTATGCTATGCTATGCTATGCT	222		
Dh	223	GGTGTGCTATGCTCCCAAAAGGCTATGCTATGCTGCTATGCTATGCTATGCTATGCT	282		
Dh	223	ATACGACGCTATATGATATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT	282		
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Dh	343	CCGT 346			
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DEFINITION	Sequence 4 from Patent EP 0088994.				
ACCESSION	U0088994				
KEYWORDS	g889447				
ORIGIN	Unknown.				
SOURCE	Unknown.	</			

QY	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675
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[illegible]

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TITLE      Direct Submission
JOURNAL    Submitted (06-FEB-197). Biological Sciences, University of
FEATURES   Nebraska, 315 Mantel Hall, Lincoln, NE 68588-0118, USA
SOURCE     source

          /organism='Hus musculus'
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          /cell_type='hybridoma*'
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          1. . . . 441
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BASE COUNT      108 A      109 C      113 G      113 T

ORIGIN

Query Match
Best Local Similarity 98.0% Score 132 DP 26 Length 443:
Matches 0: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Db 205 TGCTTCACGCACACCAACACAACCAACAACTTAAACCCTACACCCACCATTA 264
QY 163 TGCTTCACGCACACCAACACAACCAACAACTTAAACCCTACACCCACCATTA 222
Db 265 GATTTGTTTCCTGCCAAGCTGATACACTCAGTACGTGATGATATTCCTCAC 34
QY 323 GGCTCGATGCTCCCAACAGCTGACGTGACAGTGGTGAATATTCCTCAC 202
Db 275 ATGACGACACCTGATGACAAATTGCTGACACTTATTCGTGCAATATTCCT 384
QY 283 ATGACGACACCTGATGACAAATTGCTGACACTTATTCGTGCAATATTCCT 342
Db 385 CCGCT 388
QY 343 CCGCT 346

RESULT      8 NMISGACT1      684 bp      DNA      BOD
LOCUS       DEFINITION Mouse Ig kappa active gene Vkl1 VJ region..
ACCESSION   J005551
VERSION     g1965311
KEYWORDS    J region, V-region, complementarity determining region,
            immunoglobulin-kappa, immunoglobulin-kappa subgroup Xk-5, processed
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[illegible][illegible]



[illegible][illegible]

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BASE COUNT	80 A	70 C
		69 G
		87 T
ORIGIN		
Query Match	93.7%	Pctc 103 DB 290 Length 306;
Best Local Similarity	92.3%	Pctc No.1 Pctc 99;
Matches 133:	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
Dh	86	TGGCTTCAGCAAGCACAATGCATGAACCGTAAAGCGTTACACCATTA 147
Gy	163	TGGCTTCAGCAAGCACAATGCATGAACCGTAAAGCGTTACACCATTA 222
Dh	148	GATTTCCTGCTGCCCAAGGCTGACGCTGACGCTGGCGGATATATTCGAC 207
Gy	223	GCTTCCTGCTGCCCAAGGCTGACGCTGACGCTGGCGGATATTCGAC 282
Dh	208	ATTCAGACACTTGA 221
Gy	283	ATTCAGACACTTGA 286

[illegible]

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   76 g
   85 t

BASE COUNT      81 a      79 c
ORIGIN      Chromosome 6.

Query Match
Best local similarity 33.8%
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dh 111 GCAATGACATTAAGCGCATATTTTTCGCGCATCAAGTTATTCGATCCCAAAAG 180
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Dh 121 GCGATGACATTAAGCGCATATTTTTCGCGCATCAAGTTATTCGATCCCAAAAG 243
|||||
Qy 184 GCGCATATTAAGCGCATATTTTTCGCGCATCAAGTTATTCGATCCCAAAAG 243
|||||
Dh 181 TTCAATGACATTAAGCGCATATTTTTCGCGCATCAAGTTATTCGATCCCAAAAG 240
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Qy 244 TTCAATGACATTAAGCGCATATTTTTCGCGCATCAAGTTATTCGATCCCAAAAG 303
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Dh 243 GATTTCGACATTAAGCGCATATTTTTCGCGCATCAAGTTATTCGATCCCAAAAG 283
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Qy 304 GATTTCGACATTAAGCGCATATTTTTCGCGCATCAAGTTATTCGATCCCAAAAG 346
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RESULT 17
DEFINITION Mus musculus cell line C3H/72-15) chromosome 6 anti-DNA antibody
118667
ACCESSION U0500293
KEYWORDS house mouse.

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FEATURES	Location/Qualifiers
Source	"/organism="Mus musculus"
	"/strain="BALB/c"
	"/sub_species="domesticus"
	"/taxon="10990"
	"/product="immunoglobulin light chain"
	"/codon_start=1"
	"/xref="PIR:d106870"
	"/translation="SLINGAPGQYKMGKSSKSSLSHSPKRYLAVNGQVQVPLIYSVETGEGVPRFISGGSDPTLISVQADALDYFQCOHISPTTGGRRLIYRQADAPVETIPSPSSDITSGASVCFCLNFTNPDIVNFKIDSSINQNVNLS"
	"/db_xref="GenBank:U000835.1;EMBL:U000835.1;Fasta:U000835.1"
BASE COUNT	181 A 158 C 142 G 117 T
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Query Match	19 84: Score 86: DB 39: Length 618:
Best Local	Similarity 100.0%: E=0.0: S=342-70.0: Indels 0: Gaps 0:
Matches	86: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Dh	215 CTCCTGACACCTCTCGAGGGGACACACCTGGAAATAAAGCGGCGATACATGACACCA 314
Qy	341 CTCCTGACACCTCTCGAGGGGACACACCTGGAAATAAAGCGGCGATACATGACACCA 400
Dh	335 CTCGATCCACCTCCGACACACACCTG 360
Qy	401 CTCGATCCACCTCCGACACACACCTG 426
RESULT	28 IMM19802 422 bp mRNA ROD 22-NOV-1986
DEFINITION	Mus musculus strain A-B of human Cytoesglowline
ACCESSION	U000835.1
KEYWORDS	immunoglobulin VL chain mRNA, partial cds.
ORIGIN	91680672
SOURCE	house mouse,
ORGANISM	Mus musculus
REFERENCE	Birkayev, mitochondrial eukaryotes; Metazoa; Chordata;
ATTORNS	Metazoa; Eutheria; Rodentia; Sciurognathi; Muridae;
TITLE	1 (bases 1 to 423)
JOURNAL	Schoppel,K., Haefliger,E., Britt,W., Ohlin,M., Borrebaeck,C.A.N.
MEDLINE	and Much,M. specific for the antigenic domain 1 of glycoprotein B (gpB55) of human cytomegalovirus bind to different substructures
	Virology 216 (1), 133-145 (1996)
	96187797

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TITLE	JOURNAL	DATE	REFERENCE	AUTHORS	ORIGIN
Antibodies specific for the antigenic domain I of glycoprotein B (gp155) of human cytomegalovirus bind to different substructures	Journal of Virology	1986	96:187-92	16 (11), 133-145 (1986)	2 (class 1 to 438)
Direct demonstration of the presence of the antigenic domain I of glycoprotein B (gp155) of human cytomegalovirus in human placental tissue	Journal of Virology	1985	59:100-105	Schoppell, R.	Germany
Location/Qualifiers					
Location: "Mus musculus"					
Qualifier: "Salivary gland"					
Note: monoclonal antibody 27-287					
Indexing					
1. 438					
2. 438					
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REFERENCE		2 (base 1 to 423)
AUTHORS	Schoppert,K.	
JOURNAL	Journal of Molecular Evolution	
VOLUME	Submittal No.195	
PAGES	University Erlangen-Nuremberg, Schlossgarten 4., 91054 Erlangen, Germany	
FEATURES		
SOURCE	Location/Qualifiers	
	/organism='Hus musculus'	
	/strain='Balb/c'	
	/note='monoclonal antibody 27-156'	
CDS	1..443 taxon 10090	
	/product='anti-glycoprotein-B of human Cytomegalovirus immunoglobulin VL chain /translation='KSTPRLTLMWGGCTDWDVSPSSGLANRATGRTTGSGSL LVSQGVNLAAYCGKGPPLITLVMTSGEGVPAPGSCGTDTLTISVAVDL LVYCGQVRRYRFGPGGTELRNALPAFVSIPPS'	
BASE COUNT	111 a 105 c 104 g 105 t	
ORIGIN		
Query Match	Score 85; DB 29; Length 423;	
Local Similarity	100.0%;	
Matches	85% conservative 0; Homologues 0; Indels 0; Gaps 0;	
Db	338 TCCGCATTCCTCAGACGGGACCAACCATGAAATTAACGCCGTCAACGAC 398	
Gy	342 TCCGATCATCTTCACAGGGGACCAACCATGAATAAACGGCGTCAACTCACAC 401	
Dp	399 TGATCAATCTTCCACATCAACGAG 423	
Gy	402 TGATCAATCTTCCACATCAACGAG 426	
RESULT	29	
DCUS	KMGJ3903	438 bp mRNA ROD
DEFINITION	Humaneucubus anti-glycoprotein-B of human Cytomegalovirus	22-NOV-1996
ACCESSION	U13903	U13903
NID	9150674	
ORGANISM	house mouse,	
SOURCE	Eukaryotes	
REFERENCE	Eukaryotes mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euhelina; Rodentia; Sciurognathi; Muridae; Musinae; 1 (bases 1 to 438) Schoppert,K., Esserfurher,E., Bittl,W., Ohlin,M., Borrebaeck,C.A. and Mach,M.	

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	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	JOURNAL	TITLE	DATE
1	1 (bases 1 to 471)	Lester, J. J., Pelligrini, M., Souchon, R., Telio, D., Poljak, R. J., Peterson, K. C., Greene, M. I., and Alizadeh, P. M.	Characterization of a novel cross-reaction complex between Fab Ig.3.7 and Guinea-pig IgG1	J. Biol. Chem. (1995) In press	2	1 (bases 1 to 471)		
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112</								



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 402 TGTATCACTTCACATCACTCACT 436

RESULT 34 MUSICKA 943 bp mRNA ROD 12-JUN-1993  
 LOCUS mouse Ig kappa mRNA from mopc21 & other myeloma mra 3  
 DEFINITION untranslated regions.  
 ACCESSION J00550 J00552 J00600  
 KEYWORDS C-region: J-region: V-region: complementarity determining region: framework region: hypervariable region: immunoglobulin light chain: immunoglobulin-kappa: immunoglobulin kappa subgroup vk-19; mouse cDNA to myeloma mopc21 mra; cDNA to myeloma p3 (derived from mopc21) mra; cDNA to myeloma mopc19 mra; cDNA to myeloma mopc4, mopc603, a107 & hpc76 mra (see comment).  
 SOURCE Mra musculus  
 ORGANISM Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 899 to 943) Carterwright E.N., Jarvis J.M. and Haskins J.P., Brownlee G.C., Cheng C.C., Galt M.J. and Milstein C. Sequence analysis of immunoglobulin light chain messenger rna Nature 252, 354-359 (1974)  
 JOURNAL 2 (bases 857 to 943) Haskins J.P., Galt M.J., Galt M.J. and Milstein C. Immunoglobulin light chain messenger rna Nature 252, 354-359 (1974)  
 JOURNAL 3 (bases 412 to 943) Haskins J.P., Brownlee G.C., Cheng C.C., Galt M.J. and Milstein C. Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the diideoxynucleotide method of RNA sequencing Cell 15, 1067-1075 (1978)  
 JOURNAL 79084137  
 REFERENCE 4 (bases 607 to 943) Selinger C.K., Haskins J.P. and Leder P. Immunoglobulin light-chain structural gene sequences cloned in a bacterial plasmid Nature 271, 582-585 (1978)  
 JOURNAL 8064137  
 REFERENCE 5 (bases 841 to 943) Gough N.M., Cory S. and Adams J.M. Identical 3' non-coding sequences in five mouse Ig kappa chain mrae favour a unique c-kappa gene Nature 261, 594-596 (1979)

|||||  
 402 TGTATCACTTCACATCACTCACT 436

RESULT 35 MUSICKA 943 bp mRNA ROD 02-FEB-1995  
 LOCUS mouse Ig kappa mRNA from mopc21 & other myeloma mra 3  
 DEFINITION untranslated regions.  
 ACCESSION J00550 J00552 J00600  
 KEYWORDS C-region: J-region: V-region: complementarity determining region: framework region: hypervariable region: immunoglobulin light chain: immunoglobulin-kappa: immunoglobulin kappa subgroup vk-19; mouse cDNA to myeloma mopc21 mra; cDNA to myeloma p3 (derived from mopc21) mra; cDNA to myeloma mopc19 mra; cDNA to myeloma mopc4, mopc603, a107 & hpc76 mra (see comment).  
 SOURCE Mra musculus  
 ORGANISM Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 899 to 943) Carterwright E.N., Jarvis J.M. and Haskins J.P., Brownlee G.C., Cheng C.C., Galt M.J. and Milstein C. Sequence analysis of immunoglobulin light chain messenger rna Nature 252, 354-359 (1974)  
 JOURNAL 2 (bases 857 to 943) Haskins J.P., Galt M.J., Galt M.J. and Milstein C. Immunoglobulin light chain messenger rna Nature 252, 354-359 (1974)  
 JOURNAL 3 (bases 412 to 943) Haskins J.P., Brownlee G.C., Cheng C.C., Galt M.J. and Milstein C. Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the diideoxynucleotide method of RNA sequencing Cell 15, 1067-1075 (1978)  
 JOURNAL 79084137  
 REFERENCE 4 (bases 607 to 943) Selinger C.K., Haskins J.P. and Leder P. Immunoglobulin light-chain structural gene sequences cloned in a bacterial plasmid Nature 271, 582-585 (1978)  
 JOURNAL 8064137  
 REFERENCE 5 (bases 841 to 943) Gough N.M., Cory S. and Adams J.M. Identical 3' non-coding sequences in five mouse Ig kappa chain mrae favour a unique c-kappa gene Nature 261, 594-596 (1979)

|||||  
 402 TGTATCACTTCACATCACTCACT 436

RESULT 36 MUSICKA 1101 bp mRNA ROD 18-SEP-1996  
 LOCUS mouse Ig single-chain antibody mra, complete cda.  
 DEFINITION mouse Ig single-chain antibody mra, complete cda.  
 ACCESSION J00550 J00552 J00600  
 KEYWORDS C-region: J-region: V-region: complementarity determining region: framework region: hypervariable region: immunoglobulin light chain: immunoglobulin-kappa: immunoglobulin kappa subgroup vk-19; mouse cDNA to myeloma mopc21 mra; cDNA to myeloma p3 (derived from mopc21) mra; cDNA to myeloma mopc19 mra; cDNA to myeloma mopc4, mopc603, a107 & hpc76 mra (see comment).  
 SOURCE Mra musculus  
 ORGANISM Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1101) Haskins J.P., Brownlee G.C., Cheng C.C., Galt M.J. and Milstein C. Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the diideoxynucleotide method of RNA sequencing Cell 15, 1067-1075 (1978)  
 JOURNAL 79084137  
 REFERENCE 4 (bases 607 to 943) Selinger C.K., Haskins J.P. and Leder P. Immunoglobulin light-chain structural gene sequences cloned in a bacterial plasmid Nature 271, 582-585 (1978)  
 JOURNAL 8064137  
 REFERENCE 5 (bases 841 to 943) Gough N.M., Cory S. and Adams J.M. Identical 3' non-coding sequences in five mouse Ig kappa chain mrae favour a unique c-kappa gene Nature 261, 594-596 (1979)

|||||  
 402 TGTATCACTTCACATCACTCACT 436

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 KEYWORDS C-region: J-region: V-region: complementarity determining region: framework region: hypervariable region: immunoglobulin light chain: immunoglobulin-kappa: immunoglobulin kappa subgroup vk-19; mouse cDNA to myeloma mopc21 mra; cDNA to myeloma p3 (derived from mopc21) mra; cDNA to myeloma mopc19 mra; cDNA to myeloma mopc4, mopc603, a107 & hpc76 mra (see comment).  
 SOURCE Mra musculus  
 ORGANISM Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1101) Haskins J.P., Brownlee G.C., Cheng C.C., Galt M.J. and Milstein C. Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the diideoxynucleotide method of RNA sequencing Cell 15, 1067-1075 (1978)  
 JOURNAL 79084137  
 REFERENCE 4 (bases 607 to 943) Selinger C.K., Haskins J.P. and Leder P. Immunoglobulin light-chain structural gene sequences cloned in a bacterial plasmid Nature 271, 582-585 (1978)  
 JOURNAL 8064137  
 REFERENCE 5 (bases 841 to 943) Gough N.M., Cory S. and Adams J.M. Identical 3' non-coding sequences in five mouse Ig kappa chain mrae favour a unique c-kappa gene Nature 261, 594-596 (1979)

JOURNAL	Virology (1996) In press
REFERENCE	2 (bases 1 to 1101)
TITLES	Bason P Submission
STRINGS	Submitted (30-NOV-1996) Peter W. Mason, Foot-and-Mouth Disease Research Unit, USDA/ARS/NAH/PID/C, Greenport, NY 11944, USA
JOURNAL	
FEATURES	Location/Qualifiers
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v-region	64..439
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Dn	738 TCCGTCACCTCCGACGGGGGACGACGTGAATTAAAGCATGGCTGCACAC 797
Oy	342 TCCGTCACCTCCGACGGGGGACGACGTGAATTAAAGCATGGCTGCACAC 401
Dn	798 TCATGATCTTCGACACACACGCT 822
Oy	402 TCATGATCTTCGACACACACGCT 426
LOCUS	37 107188 639 bp
DEFINITION	Sequence 3 from Patent EP 0338767.
ACCESSION	I07188 PAT 14-NOV-1994

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MID          9689917
KEYWORDS     Unknown
SOURCE       Unpublished
ORGANISM     Unclassified
REFERENCE    1 (bases 1 to 639)
AUTHORS     Beavers,I.S., Sumo,T.P., Gadek,R.A. and Weigel,B.J.
TITLE       Molecular recognition and chimeric antibodies directed against a human
JOURNAL     Patent: EP 033975-A2; 3-DEC-OCT-1989;
FEATURES
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Qz           343 CCAGACGTGGGAGGCGGACCATCACTGGATAAAAAGCGGCTAATTCGACACTT 402
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Db           340 GTATCACATTGCCAACATCCACT 363
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Qy           403 GTATCACATTGCCAACATCCACT 426
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RESULT      38
LOCUS       HM001356             436 bp      mRNA                      ROD                11-NOV-1998
DEFINITION Mus musculus mRN for H3 specific immunoglobulin kappa chain, variable region, partial.
ACCESSION   J1860516
KEYWORDS    MID
            immunoglobulin superfamily; kappa chain; variable region; house mouse.
ORGANISM   Mus musculus
            Mus musculus, Chordata, vertebrates; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 436)
AUTHORS     Wetzlar,H.G., Brown,E.B., Daniels,R.S., Douglas,A.R., Skehel,J.J.
TITLE       X-ray crystallography of influenza haemagglutinin-mono-clonal antibody complexes
JOURNAL     Unpublished
            2 (bases 1 to 436)
PUBMED     Direct Submission
INSTRUMENT DNA Sequencer
LAB        Institute for Medical Research, The Ridgeway, Mill Hill, London,

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Matches:	83; Conservative:	0; Mismatches: 0; Indels: 0; Gaps: 0;
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Dy	414	TGATATCATCTTCCCACATCCA 436
Oy	402	TGATATCATCTTCCCACATCCA 424
SEQUENT 39		
LOCUS AF003299	331 bp	mRNA ROD 24-JAN-1998
DEFINITION Mus musculus 19C kappa light chain variable region mRNA, partial cds.		
ACCESSION AF003299		
KEYWORDS house mouse,		
SOURCE		
ORGANISM Mus musculus		
IDENTIFICATION Rodentia: Sciurinae: Chenidae: Vesperugo: Murinae: Muridae: Eutheria: Rodentia: Sciurinae: Muridae: Murineae: Murinae: Murus		
REFERENCE 1 (bases 1 to 321)		
AUTHORS Dittich R.D. and Schulte P.G.		

JOURNAL	antibodies	375-95-111 (1986)
REFERENCE	2	(bases 1 to 321)
AUTHORS	Ulrich H.D., Moore P.L. and Schulte P.G.	
TITLE	Germ-line diversity within the mouse Ixk-Vg gene family	
JOURNAL	Immunogenetics	47 (1), 91-95 (1998)
REFERENCE	3	(bases 1 to 321)
AUTHORS	Ulrich H.D. and Schulte P.G.	
TITLE	Direct Substitution	
JOURNAL	Submitted (09-MAR-1992) NMR, Universitat Heidelberg, Im Neuenheimerfeld 320A, D-69120 Heidelberg, Germany	
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source	1..321	
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Oy	210 CATGCCCAAAAGGTTCACGCAGCAGCATGTCGTGGCGCATATATTCCTCACACATACACA 289	
Dh	230 GGCTGATGCTTGAAGAATTTC 250	
Oy	290 GGCTGATGCTTGAAGAATTTC 310	
LOCUS	NM02052 379 bp mRNA	ROD
DEFINITION	Mus musculus polyclastic autoantibody, Immunoglobulin light chain	13-FEB-1997
ACCESSION	D02522	
KEYWORDS	mRNA, partial cde.	
ENTRY	91438584	
REMARKS	.	

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Dy	346	TACATCTTCCGAGGGGAGGACACACGATGAAATTAAGAGCGTCAATCTGTCGACACATGTA	405		
Dh	355	TACATCTTCCGAGGGGAGGACACACGATGAAATTAAGAGCGTCAATCTGTCGACACATGTA	405		
Dy	406	TCCATCTTCCGAGGGGAGGACACACGATGAAATTAAGAGCGTCAATCTGTCGACACATGTA	426		

RESULT	41	729 bp	mRNA	ROD	07-MAY-1997	
DEFINITION		Pajunen, M.I., Sevriyeva, N.P. and Karp, M. Immunoglobulin aberrantly rearranged kappa chain RNA partial sequence.				
ACCESSION		U05414				
WID		9207212				
ORGANISM		house mouse				
SOURCE		Mus musculus				
REFERENCE		Eukaryotes: mitochondrial eukaryotes; Metazoa, Chordata; Vertebrates: Mammalia; Eutheria; Rodentia; Soturognathi; Muridae; 1 (bases 1 to 729)				
REFERENCE		Pajunen, M.I., Sevriyeva, N.P. and Karp, M. Immunoglobulin aberrantly rearranged kappa-chain-mRNA (bases 1 to 729)				
REFERENCE		Pajunen, M.I., Sevriyeva, N.P., Jaurila, P., Karp, M., Pettersson, K., Direct Substitution (1995) M. I. Pajunen, Nuth Centre for Biotechnology, P.O. Box 133, Helsinki, FIN-00013 Finland				
COMMENT		Carroll, W. L. Mol. Immunol. 25, 991-995, 1988				
FEATURES		Kallene, B. Gene 122, 331-338, 1992. Location/Qualifiers				
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Db	316	TACAGCTCGGAGCGGCGGACACAGCTGCAATATTAACGGCGCTATATCGTCACGACACTCTA	395			
Db	346	TACAGCTCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	405			
Db	396	TCCATCTTCCGACACGACGAT	416			
Qy	406	TCCATCTTCCGACACGACGAT	426			
RESULT	42					

LOCUS	MM101a	882 bp	RNA	ROD	30-SEP-1993
DEFINITION	Immunoglobulin mRNA for monoclonal antibody light chain kappa.				
DESCRIPTION					
KEYWORDS	immunoglobulin kappa light chain.				
NUM	9406234				
NUM	9406234				
SOURCE	house mouse.				
ORGANISM	Mus musculus.				
REFERENCE	1. (bases 1 to 882)				
REFERENCE	Verhebraak, A.therbert, Rodentia, Sciencemich, Myomyspina, Muridae.				
JOURNAL	Biorinne: Mus.				
AUTHORS	2 (bases 1 to 882)				
TITLE	Direct Submission				
JOURNAL	Ducancel, F.P.D.				
FEATURES	Location/Qualifiers				
source	1..882				

Query Match	18 63	Score 81	DB 29	Length 882
Best Local Similarity 100.00				
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[illegible]

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Db	CCGCAAAAGCGTGAACAGCAGATGATGGCTAATTATTCGACATGCAGAGCCT 233
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REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE
1	Chen, J.H., Kunkle, C.L., Nguyen, K.A., Cation, A.V., and Etkin, J.	Characterization of a B cell tolerance in a mouse model of systemic lupus	J. Exp. Med.	181 (3), 1157-1167 (1995)	95175583
2	(bases 1 to 246)				
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[illegible]

AUTHORS	Roark,J.H.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1995) Jessica H. Roark, Matar Institute, 3601 Space St., Location/Omiffers 1104, USA
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CDS	1..246 "/organism=Mus musculus" /strain=MDL-169/ /DB=NCBI/MDL169/ /clone=MDL169/ /cell_type=splenic B cell hybridoma/ /tissue_type=splenic <1..246 adult /codon_start=1 product=immunoglobulin kappa light chain variable region /cdate=PID:681989. /translation=CAGACDGGSLALGQSPDTRELIATRLSDGPVSCGR SGSDSIILSSLEPPDYDTQQGSEPLTPMATGL
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Gy 219 AAMCGCTAATGCAATGTCGTGCAGCATTTATTCCACACAGCAGCCCTTACT 298	
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Gy 299 CTGAATAATTCTTG 313	
RESULT 49	
LOCUS	MMDJ19327 261 bp mRNA ROD 21-JUN-1995
DEFINITION	Mouse immunoglobulin kappa light chain variable region mRNA,
ACCESSION	U19327
NID	9619990
SOURCE	house mouse,
ORGANISM	Mus musculus
REFERENCE	Eukaryotes; alveochondriat eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Myomorpha; Muridae;
AUTHORS	Roark,J.H., Kuntz,G.L., Nguyen,K.A., Cason,A.J. and Erikson,J.
TITLE	Breakdown of B cell transition in a mouse model of systemic lupus

[illegible]



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Page 81

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Query Match 8 7%: Score 38; DB 24; Length 297;  
 Ectoderm 100.0%; Pred. No. 2,656-50;  
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BASE COUNT 84 a 94 c 83 g 88 t 3 others  
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 Adams,M.D., Kariya,A.R., Pletschmann,R.D., Pulner,R.A.,  
 Butt,C.J., Lee,N.H., Kirtress,E.F., Welstock,K.G., Goeyne,J.D.,  
 Clayton,R.A., Cline,R.A., Brandon,R.C., Man,Wai,C.,  
 Fitzgerald,L.W., Fitzhugh,W.M., Fitchman,J.T., Hughes,J.L.,  
 Glodak,A., Gnehm,C.L., Hanna,M.C., Hedlorn,E., Hinkle,P.S., Jr.,  
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Narmas,S.M., Merrick,J.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Nguyen,D.T., Pelligrino,S.M.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Wetman,J.F., Li,Y.N.,  
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 Raymond,L., Welty,F., Whang,J., Xu,C., Yu,C.L., Rubin,S.M.,  
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl.), 3-174 (1995)

AUTHORS  
 Adams,M.D., Kariya,A.R., Pletschmann,R.D., Pulner,R.A.,  
 Butt,C.J., Lee,N.H., Kirtress,E.F., Welstock,K.G., Goeyne,J.D.,  
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 Raymond,L., Welty,F., Whang,J., Xu,C., Yu,C.L., Rubin,S.M.,  
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl.), 3-174 (1995)

TITLE  
 JOURNAL  
 MEDLINE  
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 COMMENT  
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REFERENCE  
 1 (bases 1 to 352)  
 Adams,M.D., Kariya,A.R., Pletschmann,R.D., Pulner,R.A.,  
 Butt,C.J., Lee,N.H., Kirtress,E.F., Welstock,K.G., Goeyne,J.D.,  
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 Kelley,J.M., Kelley,J.C., Liu,L.-I., Narmas,S.M., Merrick,J.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Nguyen,D.T., Pelligrino,S.M.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Wetman,J.F., Li,Y.N.,  
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dume,D., Feng,D.F., Ferris,A., Fletcher,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
 Raymond,L., Welty,F., Whang,J., Xu,C., Yu,C.L., Rubin,S.M.,  
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl.), 3-174 (1995)

AUTHORS  
 Adams,M.D., Kariya,A.R., Pletschmann,R.D., Pulner,R.A.,  
 Butt,C.J., Lee,N.H., Kirtress,E.F., Welstock,K.G., Goeyne,J.D.,  
 Clayton,R.A., Cline,R.A., Brandon,R.C., Man,Wai,C.,  
 Fitzgerald,L.W., Fitzhugh,W.M., Fitchman,J.T., Hughes,J.L.,  
 Glodak,A., Gnehm,C.L., Hanna,M.C., Hedlorn,E., Hinkle,P.S., Jr.,  
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Narmas,S.M., Merrick,J.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Nguyen,D.T., Pelligrino,S.M.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Wetman,J.F., Li,Y.N.,  
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
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 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
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 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl.), 3-174 (1995)

TITLE  
 JOURNAL  
 MEDLINE  
 COMMENT  
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[illegible][illegible]

Tel.: 3018699056  
Fax: 3018699423  
E-mail: [ncicinfo@ncic.nih.gov](mailto:ncicinfo@ncic.nih.gov)  
For citation purposes, please provide additional sequence and expression information related to this EST. Please check The TIGR Human Gene Index (<http://www.tigr.org/tgh/hg/hgi.html>)  
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1-303bp/Qualifiers  
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RefSeq 18-Apr-1997

REMARKS  
LOCUS AA300788 303 bp mRNA EST  
DEFINITION Estig384 Testis tumor Homo sapiens CDNA 5' end similar to  
EMBL384 testis kappa light chain, V region, mRNA sequence.  
ACCESSION AA300788  
KEYWORDS EST  
ORGANISM human.  
Other species: Alouatta palliata, Canis lupus, Mus musculus, Oryzomys latipes,  
Peromyscus maniculatus, Rattus norvegicus, Sus scrofa, Xenopus laevis,  
Yersinia enterocolitica, Yersinia pseudotuberculosis.  
Vertebrate: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea:  
Homo.

REFERENCE  
1. (base 1 to 303)  
Bodmer W.D., Krangel A.A., Planchemann R.D., Palmer R.R.A.,  
Pridmore A.M., Bowness F., Brown D.G., Brown K.E., Collier A.C.,  
White O., Sutton C., Blake J.A., Brandon R.C., Macfarlane I.J.,  
Cleyton R.A., Clifton M., Cotton M.D., Earle-Hughes J., Fine L.B.,  
Fitzgerald M.K., Fitzsimmons W.K., Friedman J.T., Georgakilas N.S.,  
Keller J.W., Kelley C.C., Liu L.-I., Mamura S.M., Metrick J.M.,  
Moreno-Vargales R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,  
Phillips C.A., River S.E., Scott J.L., Stauder D.M., Shilley R.

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Db      59      CCNAATGTGACACACACATGACACATGTGACATGTCGC 96
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QY
RESULT 20
R14683      335 bp      mRNA      clone 1526 EST      18-MAY-1995
DEFINITION      gp:000665_cdel 10 KAPPA CHAIN PROMOTOR V 1 REGION (HUMAN)..
ACCESSION      R14683
KEYWORDS      9111783
SOURCE
human clone-1526B1 library-sources breast DMH2B vector-p772D
(pharmacia) with a modified polyclinker host-DH2B (emphillin
resistant) plasmid-pM3p1. Restr=Not I Restr=Not RI digest female
rat estrus cDNA was paired with a Not I - oligo(dT) primer [5']
double-stranded cDNA was ligated into Eco RI restriction 3' phar-macia)
digested with Not I and cloned into the Not I and Eco RI sites of
modified p773 vector (pharmacia). Library went through one round
of transformation to a Coli -350. Library constructed by Bento
Garcia and Dr. William Bonaldi.
ORGANISM      Homo sapiens
Tissue: testis
Embryonic: Metastase, Fumeralstase, Bilateralis; Coelomata;
Dermatocuticula; Choroides; Vertebrata; Gnathostomata; Osteichthyes;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Hominidae; Homo.
REFERENCE
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Hillier, L.G., Clark, R., Dubnue, T., Elliston, R., Hawkins, M.,
Parsanian, A., Riddle, R., Rong, L., Scheraga, C., Meyer, M.,
Tverskaya, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R. - March 87 Project
JOURNAL
COMMENT
Contact: Wilson R
Project: Human Genome Project
Institution: Washington School of Medicine
4444 Forbes Park Parkway, Box 5501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```

TITLE	Initial assessment of human gene diversity and expression patterns based upon 88 million nonredundant cDNA sequences					
JOURNAL	Nucleic Acids Res 317 (1994) Suppl. 3:174 (1995)					
MEDLINE	96092380					
CHECKED	Curtis, C.S.; MRC6717					
COMMENT	Genetics, Molecular Biology, and Biostatistics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Fax: 3018699423 E-mail: arkr@vtv.tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/db/hg1/mgi.html">http://www.tigr.org/db/hg1/mgi.html</a> ) Seq primer: M3 Reverse Location/Qualities 1..203 name=Homo sapiens* note=Organism: pancreas; Vector: plasmidscript SR-; Site_1: ECORI; Site_2: XhoI MD_xref: ATCC (dbest):191063 clone.lib=pancreas tumor 1* dev_stage=sadult* <1..>203 6 C 51 g 44 C 5 others					
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Method	3); conservative 0; Matrix: 1; Indels 0; Gaps 0;					
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RESULT	22					
DEFINITION	AA395508 202 bp mRNA ZST					
DESCRIPTION	EST100751 Pancreatic tumor Homo sapiens 5' end, related to immunoglobulin kappa light chain, V region, mRNA sequence.					
ACCESSION	AA395508					
KEYWORDS	91547914					
RID	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; 1 (bases 1 to 222)					

[illegible]

97 33 C:\NORTH\DATA\CDNA\BAC\CDNA000001.CC

	RESULT	33
LOCUS	A81912	510 bp mRNA EST 17-FEB-1998
DEFINITION	U1-R-40-sp-e-12-O-U1.3 similar to gpIM44(4) RABBITA P4.15 active kappa-chain mRNA VJC-region from Immunocytoam 1R2. mRNA sequence.	
ACCESSION	A81912	
KEYWORDS	9288938	
SOURCE	Norway rat.	
ORGANISM	Rattus norvegicus	
TITLE	Fukuyamae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	
REFERENCE	Rodenas; Solerogah; Nulida; Murine; Rattus.	
AUTHORS	Bonaldi,M.F., Lennon,G. and Soares,M.B.	
JOURNAL	Normalisation and subtraction: two approaches to facilitate gene discovery	
MEDLINE	9704447[see. 6 (9). 791-806 (1996)]	
COMMENT		

Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
451 Eastwin Medical Research Building Iowa City, IA 52242, USA  
Tel.: 319 335 9250  
Fax: 319 335 9555  
E-mail: msoares@iastate.edu  
The sequences are deposited to the CDNA between the most site and the oligo-dT track (not shown) served to identify it as a clone from the normalised adult Lung library. cDNA Library preparation: M.  
Petras Bonaldi, Ph.D. Clone distribution: clones will be available  
Seq primer: M3 Forward  
  
Location/Qualifiers  
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/strain="Sprague-Dawley"  
/note="Vector: pTZ19-Pac (Pharmacia) with a modified polymerase. Site1: Not I; Site2: Eco RI; This library contains a mixture of individually tagged normalized cDNAs from adult lung tissue. The following genes were identified: brain, liver, kidney, heart, spleen, ovary and muscle. The tag is a string of 3-5 nucleotides present between the normalized and the oligo-dT track which allows identification of the library of origin of a clone within the mixture."  
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RESULT	32		
DEFINITION	AJ298481	289 bp cDNA MN	EST
ACCESSION	F0101050	Panor homo sapiens EST	18-APR-1997
KEYWORDS	immunoglobulin kappa light chain, V region, mRNA sequence.		
SOURCE	G194817		
ORGANISM	human.		
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	Vertebrata; Mammalia; Eutheria; Placenta; Carnivora; Homidae;		
REFERENCE	1 (bases 1 to 289)		
AUTHORS	Adams M.D., Keizawa A.R., Fielesmann R.D., Fulmer R.A., Burt C.J., Lee S.H., Kikusa E.F., Weinstock K.C., Gogean J.D., Hill C., Sutton C., Blake J.A., Brandon R.C., Man-Wai C., Chen L., Stott O., Pitzum W.M., Friedman H., Hughes J., Fine L.O., Fitzgerald L.W., Fitzum W.M., Coleman T.A., Collins E.J., Glodak A., Gohm C.L., Hanna N.C., Hedlorn E., Hinkle S.G., Kelley J.M., Kelley J.C., Liu L.T., Marzetta S.W., Merrick J.M., Phillips-Palantque, R., McDonald L.A., Nguyen D.T., Pelligrino S.M., Pittman C., Rasmussen R., Schmitt R.S., Schmidt J., Phillips R., Small K.V., Spriggs T.A., Utterback R.S., Weidman J., Benhardt D.D., Cao J., Cepeda M.A., Coleman T.A., Collins E.J., Diack D., Fang D.-P., Ferris A., Fischer C., Hastings K.J., Dierckx D., Huynh-Geneva J.M., Gruber S., Hudson P., Kim A.K., Kosaki D., Lu-Huynh-Geneva J.M., Gruber S., Hudson P., Kim A.K., Raymond L., Wiley P., Wang J., Xu C., Yu C.L., Rubin S., Olsen H., Dillon P.J., Panon M.R., Rosen C.A., Resheff A.A., Palda C., Treier C.M. and Venter J.C.		
JOURNAL	Genomics	23	1995
COMMENT	based upon 83 million nucleotides of cDNA sequence Accession 377 (6547-177), 3-174 (1995) 9602680		
	Contig ID# : NM161717		
	Contig Length: 117 bp		
	Biotechnology		
	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850 USA		
	Tel.: 3018999423		
	Fax: 3018999423		
	Email: arretselvici@org		
	For clone availability, additional sequence and expression		
	information related to this EST, please check the TIGR Human Gene		

Mon Apr 19 13:23:50 1999

US-08-836-455-1.rst

Page 63

Mon Apr 19 13:23:50 1999

US-08-836-455-1.rtf

Page 64

	CONTACT:	FelAvargas, AR
	BIOINFORMATICS	
	906 Institute for Genomic Research	
	Genetic Center Drive, Rockville, MD 20850 USA	
	Tel.: 3016699056	
	Fax: 3016699423	
	Email: arfelavargas@igf.org	
	Keywords: availability; additional sequence and expression information	
	Index ( <a href="http://www.ncbi.nlm.nih.gov/db/hs/hsl.html">http://www.ncbi.nlm.nih.gov/db/hs/hsl.html</a> )	
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ACCESSION	U05041 Human Polio 2 KIP KAP CHAIN PROCONSOR V-I Region ;	
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[illegible]



**FEATURES**  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Other ESTs: EST19456, TNC167177  
 Contact: Kiplavage, AR  
 Biotechnology for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: kiplavage@tigr.org  
 Note: This entry contains additional sequence and expression information related to this EST. Please contact the TIGR Human Gene Seq primer: M3 Reverse.  
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 1 clone="Homo sapiens"  
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 /dev\_stage="adult"  
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Fax: 3018699423  
 Email: tdbolton@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbolton@tigr.org)  
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**FEATURES**  
 SOURCE  
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 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Other ESTs: EST19456, TNC167177  
 Contact: Kiplavage, AR  
 Biotechnology for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: kiplavage@tigr.org  
 Note: This entry contains additional sequence and expression information related to this EST. Please contact the TIGR Human Gene Seq primer: M3 Reverse.  
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 1 clone="Homo sapiens"  
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**FEATURES**  
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 Contact: Kiplavage, AR  
 Biotechnology for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
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 1..2002  
 /dev\_stage="fetal"  
**FEATURES**  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Other ESTs: EST19456, TNC167177  
 Contact: Kiplavage, AR  
 Biotechnology for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: kiplavage@tigr.org  
 Note: This entry contains additional sequence and expression information related to this EST. Please contact the TIGR Human Gene Seq primer: M3 Reverse.  
 Location/Qualifiers  
 1 clone="Homo sapiens"  
 /organism="Homo sapiens"  
 /note="Organ: esophagus; Vector: plasmid; Site: 1;"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Esophagus tumor"  
 /dev\_stage="adult"  
 1..3545







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/db_xref="ATCC (inhost):192122"
/db_xref="taxon:9606"
/clone_id="Testis tumor"
/sex="male"
/age="adult"
<1 ->353
BASE COUNT      84 a      85 g      93 t      4 other
ORIGIN
Query Match      4 43: Score 19; DB 24; Length 363;
Best Local Similarity 100.00; Pwd. No. 2.83e+07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 288 CTTCTACCAATCCAGCCCT 306
OY 275 CTTCTACCAATCCAGCCCT 293

Search completed: Sat Apr 17 16:41:45 1999
Job time : 1470 secs.
```



!!SEQUENCE LIST 1.0

(Peptide) WORDSEARCH of: /home/obryen/free455/olig/us-08-836-455-2 check: 4259 from: 1

FROMIG of: /home/obryen/free455/olig/US08836455 pep  
sequence 2, application us/08836455

general information:  
applicant: chatterjee, malaya  
applicant: toon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: pir: \* Sequences: 116,738 Total-length: 37,460,341 April 18, 1999 13:58

Database Release Information:

NBRF, Release 58.0, Released on 30sep1998, Formatted on 15dec1998

Word-size: 5 Words: 49743 Diagonals: 7,036 Total Diagonals: 54,270,613  
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 4.54

Sequence Strid Diag Score Width Documentation ..

PIR1:KYMSM4	+	2	116	1	Ig kappa chain precursor V region (MC
PIR2:PI0260	+	-20	98	1	Ig kappa chain V region (anti-DNA, DE
PIR2:PI0259	+	-20	95	1	Ig kappa chain V region (anti-DNA, DE
PIR2:PI0261	+	-38	81	1	Ig kappa chain V region (anti-DNA, DE
PIR4:BA7271	+	-19	80	1	nitrophenyl phosphate-specific anti
PIR2:PH1062	+	-20	77	1	Ig light chain V region (clone 202.10
PIR2:PI0262	+	-20	77	1	Ig kappa chain precursor V region (VK
PIR1:KYMS3B	+	2	70	1	Ig kappa chain precursor V region (VK
PIR2:BA28840	+	-26	69	1	Ig kappa chain V region (HP27) - mouse
PIR2:C28840	+	-26	66	1	Ig kappa chain V region (HP22) - mouse
PIR2:BA28840	+	-35	64	1	Ig kappa chain V region (HP29) - mouse
PIR2:SI17622	+	-28	61	1	Ig kappa chain precursor V region - mouse
PIR2:SI17622	+	2	56	1	Ig kappa chain precursor V region (BX
PIR2:DI32513	+	-14	52	1	Ig kappa chain precursor V region (ar
PIR2:JI0080	+	-3	50	1	Ig kappa chain - mouse (fragment)
PIR2:SO9365	+	2	49	1	Ig kappa chain precursor V region (IR
PIR2:BA2986	+	0	49	1	Ig kappa chain precursor V region (M-
PIR2:PH1224	+	-6	49	1	Ig kappa chain precursor V region (M-
PIR2:BA29380	+	0	49	1	Ig kappa chain V region (Ars-A) - mouse
PIR2:BA26406	+	0	49	1	Ig kappa chain precursor (15C5) - mouse
PIR2:SI14237	+	-1	47	1	Ig kappa chain precursor V region (5-
PIR2:BA3904	+	-20	47	1	Ig kappa chain (clone KL2.29 / KL2.33
PIR2:BA6903	+	-20	46	1	Ig kappa chain V region (M-T151) - mouse
PIR2:SI19970	+	-20	46	1	Ig kappa chain V region (36-71) - mouse
PIR2:BA30551	+	-20	46	1	Ig kappa chain V region (3D10) - mouse
PIR2:C26405	+	-20	45	1	Ig kappa chain V region (anti-arsone
PIR1:KYMSAR	+	-20	45	1	Ig kappa chain V region (45-49, anti
PIR2:PI0282	+	-20	45	1	Ig kappa chain V region (1F6) - mouse
PIR2:BA26405	+	-20	45	1	Ig kappa chain (clone KL2.18 / KL2.10
PIR2:BA6900	+	-20	44	1	Ig kappa chain V region (GPI) - mouse
PIR2:BA28044	+	-20	44	1	Ig kappa chain V region - mouse (frag
PIR2:SI3188	+	0	44	1	Ig kappa chain V region - mouse
PIR2:SI52447	+	-20	44	1	Ig kappa chain V region (hybridoma NC
PIR2:SI13700	+	-20	44	1	Ig kappa chain V region (anti-idiotyp
PIR2:BA5026	+	-20	44	1	Ig kappa chain V region A30 - human
PIR2:SI1809	+	-6	44	1	Ig kappa chain V-J region - human
PIR2:SI40313	+	-4	44	1	Ig kappa chain V-J region - human
PIR2:SI40313	+	-4	44	1	Ig kappa chain V region (22B5) - mouse
PIR2:BA28044	+	-20	43	1	Ig kappa chain V region (anti-cyclosp
PIR2:PH0807	+	-20	42	1	Ig kappa chain - human (fragment)
PIR2:SI1979	+	-20	42	1	Ig kappa chain V region (24) - mouse
PIR2:DA4677	+	0	41	1	Ig kappa chain V-J region (44.1) - mouse
PIR2:SI01320	+	-20	41	1	Ig kappa chain V-J region (48) - mouse
PIR2:BA4677	+	-20	41	1	Ig kappa chain - human (fragment)
PIR2:SI1980	+	-20	40	1	Ig kappa chain V region (clone NQ5-83
PIR2:SI1983	+	-20	40	1	Ig kappa chain V region (hybridoma NC
PIR2:SI1124	+	-20	40	1	Ig light chain V-J region (419.1) - pi
PIR2:SI13703	+	-20	40	1	Ig kappa chain - human
PIR2:CA4677	+	-20	40	1	Ig kappa chain - human
PIR2:SI40369	+	1	40	1	Ig kappa chain - human

at least 5 aa long

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ACCESSIONS PC4203  
REFERENCE Rakt, V.W.; Lee, D.I.; Choi, B.K.; Cho, M.K.; Lee, S.H.;  
#authors  
#journal Gene (1996) 173:257-259  
#title Cloning and characterization of cDNAs coding for heavy and  
light chains of a monoclonal antibody (MAb43) specific for  
human plasma apolipoprotein A-I.  
#accession PC4203  
#molecule-type mRNA  
#residues 1-219 #label RNA  
#cross-reference DB 029147; NID:9159423; PID:91594226  
COMMENT This protein is specific for human plasma apolipoprotein A-I of  
#protein high density lipoprotein.  
FEATURES  
1-112  
#domain V region status predicted #label VAR\  
#domain C region status predicted #label CRO  
#length 219 checksum 5881  
SUBMARY  
Query Match 17.9% Score 26; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 1,67e-42;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 107 TRGCGTLETRKADAPVPSIPSS 127  
QY 117 TRGCGTLETRKADAPVPSIPSS 142

RESULT 12  
ENTRY S18855 #type fragment  
#protein Ig kappa chain - mouse (fragment)  
#organism Mus musculus  
#date 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change  
10-Sep-1997  
ACCESSIONS S18855  
#authors Kipp, B.; Becker, M.; Schlack, M.  
#description Submitted to the EMBL Data Library, November 1993  
#submission Combination of a defined specificity and desired isotype by  
cloning of an anti ovalbumine recombinant mouse 1991/19E  
#accession S18855  
#status preliminary  
#molecule-type mRNA  
#residues 1-219 #label KIP  
#cross-reference EMBL:375139; NID:9141638; PID:9141639  
#organism Mus musculus  
#date 10-Sep-1997  
SUBMARY  
Query Match 17.9% Score 26; DB 2; Length 219;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 117 TRGCGTLETRKADAPVPSIPSS 142

RESULT 14  
ENTRY PR0445 #type fragment  
#protein Ig kappa chain precursor V-I region - human (fragment)  
#organism Homo sapiens  
#date 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change  
16-Aug-1996  
ACCESSIONS PR0445  
#authors D.H.; Betzel, G.; Shao, H.; Diamantstein, T.; Weidte,  
#journal Gene (1992) 122:321-328  
#title A general method for characterization of monoclonal antibodies  
by inverse polymerase chain reaction which conserves  
the complete N-terminal sequences.  
#accession PR0445  
#molecule-type mRNA  
#residues 1-128 #label KAL  
#cross-reference EMBL:375137; NID:9141637; PID:9141636  
#organism Homo sapiens  
#date 30-Sep-1993  
SUBMARY  
Query Match 15.2% Score 22; DB 2; Length 128;  
Best Local Similarity 100.0%; Pred. No. 1,41e-32;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 107 TRGCGTLETRKADAPVPSIP 128  
QY 117 TRGCGTLETRKADAPVPSIP 138

RESULT 15  
ENTRY PR0446 #type fragment  
#protein Ig kappa chain precursor V-II region - human (fragment)  
#organism Homo sapiens  
#date 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change  
16-Aug-1996  
ACCESSIONS PR0446  
#authors Kalusa, B.; Betzel, G.; Shao, H.; Diamantstein, T.; Weidte,  
#journal Gene (1992) 122:321-328  
#title A general method for characterization of monoclonal antibodies  
by inverse polymerase chain reaction which conserves  
the complete N-terminal sequences.  
#accession PR0446  
#molecule-type mRNA

Best Local Similarity 100.0%; Pred. No. 1,67e-42;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 107 TRGCGTLETRKADAPVPSIPSS 127  
QY 117 TRGCGTLETRKADAPVPSIPSS 142

RESULT 13  
ENTRY J10029 #type fragment  
#protein Ig kappa chain precursor (RP93) - mouse (fragment)  
#organism Mus musculus  
#date 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change  
22-Nov-1996  
ACCESSIONS J10029  
#authors M.C.; Pollock, R.R.; Desjardins, C.; Schmitt, M.D.  
#journal J. Exp. Med. (1998) 167:954-973  
#title Point mutations cause the somatic diversification of IgM and  
#cross-reference EMBL:375135  
#accession J10029  
#molecule-type mRNA  
#residues 1-225 #label CHI  
#cross-reference EMBL:375135; NID:9141413; PID:9141414  
#organism Mus musculus  
#date 31-Dec-1993  
SUBMARY  
Query Match 15.2% Score 22; DB 2; Length 217;  
Best Local Similarity 100.0%; Pred. No. 1,41e-32;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 104 GTRLETRKADAPVPSIPSS 125  
QY 121 GTRLETRKADAPVPSIPSS 142

RESULT 17  
ENTRY S14337 #type complete  
#protein Ig kappa chain precursor (1955) - mouse  
#organism Mus musculus  
#date 25-Feb-1994 #sequence-revision 10-Nov-1995 #text-change

RESULT 16  
ENTRY S43772 #type complete  
#protein Ig kappa chain - mouse  
#organism Mus musculus  
#date 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change  
16-Aug-1996  
ACCESSIONS S43772  
#authors Schalken, C.A.  
#journal Submitted to the EMBL Data Library, November 1993  
#description  
#accession S43772  
#molecule-type mRNA  
#residues 1-217 #label SCH  
#cross-reference EMBL:375136; NID:9141413; PID:9141414  
#organism Mus musculus  
#date 06-Jan-1995  
SUBMARY  
Query Match 15.2% Score 22; DB 2; Length 217;  
Best Local Similarity 100.0%; Pred. No. 1,41e-32;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 104 GTRLETRKADAPVPSIPSS 125  
QY 121 GTRLETRKADAPVPSIPSS 142

RESULT 17  
ENTRY S14337 #type complete  
#protein Ig kappa chain precursor (1955) - mouse  
#organism Mus musculus  
#date 25-Feb-1994 #sequence-revision 10-Nov-1995 #text-change

ACCESSIONS 514237  
514236  
AUTHORS Vandamme, A.M.; Bulens, F.; Bernat, H.; Welles, L.; Lijnen, F.R.; Collen, D. (1990) 192:767-775  
JOURNAL Biochem. J. (1990) 192:767-775  
TITLE Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.  
cross-references: MIM:3106173  
#molecule\_type mRNA  
#residues 1-234 #label VAN  
#cross-references: EMBL:X56394; NID:951623; PID:951623  
KEYWORDS Estimer, Immunoglobulin 26087; Echeckum 6000  
SDRAWR Length 219; Molecular-weight 26087; Echeckum 6000  
Query Match 15.24; Score 22; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.0e-37;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 121 GTRKLRADAPVTSIPPS 142  
CY 121 GTRKLRADAPVTSIPPS 142

RESULT 18  
ENTRY C28840  
#type fragment  
#formal\_name 1g kappa chain V region (BP2) - mouse (fragment)  
ORGANISM Mus musculus  
DATE 29-Aug-1987; sequence\_revision 29-Aug-1987; text\_change 16-Aug-1996  
ACCESSIONS C28840; J25114  
REFERENCES Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Pongereau, M.  
JOURNAL EMBO J. (1985) 4:3681-3688  
TITLE The idiotype network and the internal image: possible (anti-idiotypic) antibodies in the GAT system.  
cross-references: MIM:86136012  
#accession C28840  
#molecule\_type mRNA  
#residues 1-110 #label OIL  
CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology  
SDRAWR heterotrimer; Immunoglobulin  
Length 101; Echeckum 5983  
Query Match 13.84; Score 20; DB 2; Length 101;  
Best Local Similarity 90.9%; Pred. No. 1.0e-27;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REFERENCE A01028  
AUTHORS Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Pongereau, M.  
JOURNAL EMBO J. (1985) 4:3681-3688  
TITLE The idiotype network and the internal image: possible (anti-idiotypic) antibodies in the GAT system.  
cross-references: MIM:86136012  
#accession B28840  
#molecule\_type mRNA  
#residues 1-110 #label OIL  
CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology  
SDRAWR heterotrimer; Immunoglobulin  
Length 101; Echeckum 7015  
Query Match 13.14; Score 19; DB 2; Length 101;  
Best Local Similarity 90.5%; Pred. No. 2.50e-25;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
DB 80 YICQASPTTGGCTTET 100  
CY 106 YICQASPTTGGCTTET 126

RESULT 21  
ENTRY A56169  
#type fragment  
TITLE 1g kappa chain V region (clone 23.2) - mouse (fragment)  
ORGANISM Mus musculus  
DATE 19-Oct-1995; sequence\_revision 19-Oct-1995; text\_change 15-Aug-1996  
ACCESSIONS A56169  
REFERENCES Montfardin, C.; Kleber-Emons, T.; vonFelde, J.M.; O'Malley, D.; Rothenbaum, R.; Doolittle, A.P.; Kaushansky, K.; Brown, W.V.; Voeck, D.; McCallum, D.R.; Weidner, D.B.; Williams, J. Biol. Chem. (1995) 270:6628-6638  
TITLE Recombinant antibodies in bioactive peptide design.  
ABSTRACT Preliminary: not compared with conceptual translation  
#status preliminary  
#molecule\_type mRNA  
#residues 1-210 #label MOX  
KEYWORDS heterotrimer; Immunoglobulin  
SDRAWR Length 210; Echeckum 4986  
Query Match 13.14; Score 19; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 2.50e-25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 108 LTRRADAPVTSIPPS 126  
CY 108 LTRRADAPVTSIPPS 126

DB 80 YICQASPTTGGCTTET 101  
CY 106 YICQASPTTGGCTTET 127

RESULT 19  
ENTRY P10262  
#type fragment  
TITLE 1g kappa chain V region (anti-DNA, 60V) - mouse (fragment)  
ORGANISM Mus musculus  
DATE 16-Sep-1996; sequence\_revision 16-Sep-1992; text\_change 16-Aug-1996  
ACCESSIONS P10262  
REFERENCES Shalovich, K.; MacCall, M.; Shan, H.; Radic, M.Z.; Plascaky, J. Exp. Med. (1990) 171:265-282; J. Biol. Chem. (1990) 265:282-287.  
TITLE Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
cross-references: MIM:30011618  
#accession P10262  
#molecule\_type mRNA  
#residues 1-106 #label SHL  
CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology  
SDRAWR heterotrimer; Immunoglobulin  
Length 106; Echeckum 658  
Query Match 13.84; Score 20; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.0e-27;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 64 GRSQSDYSLTSLSEEDY 83  
CY 84 GRSQSDYSLTSLSEEDY 103

RESULT 20  
ENTRY B28840  
#type fragment  
TITLE 1g kappa chain V region (BP2) - mouse (fragment)  
ORGANISM Mus musculus  
DATE 29-Aug-1987; sequence\_revision 29-Aug-1987; text\_change 16-Aug-1996  
ACCESSIONS B28840; J25114

CY 124 LTRRADAPVTSIPPS 142

RESULT 22  
ENTRY S16112  
#type complete  
TITLE 1g kappa chain V region (Ga) - mouse  
ORGANISM Mus musculus  
DATE 21-Nov-1993; sequence\_revision 10-Nov-1995; text\_change 16-Aug-1996  
ACCESSIONS S16112  
REFERENCES Vignery, M.; Proulx, M.; Weisgerber, C.; Eckart, K.; Kretzlin, H.; Bitter-Suermann, D.; Hillebrand, N.; Bitter-Suermann, D.; Hoppe-Seyler, (1991) 372:451-453  
TITLE Primary structure of the murine monoclonal IgG2a antibody MA613 (antigen alpha(2)-microglobulin) polypeptide chain. Amino acid sequence, cDNA sequence, and 1987 (47) chain. Nucleic Acids. Res.  
cross-references: MIM:3200033  
#accession S16112  
#status preliminary  
#molecule\_type mRNA  
#residues 1-219 #label BIT  
KEYWORDS heterotrimer; Immunoglobulin  
SDRAWR Length 219; Molecular-weight 24216; Echeckum 7375  
Query Match 13.14; Score 19; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 2.50e-25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 109 LTRRADAPVTSIPPS 127  
CY 124 LTRRADAPVTSIPPS 142

RESULT 23  
ENTRY S53028  
#type complete  
TITLE 1g kappa chain - mouse  
ORGANISM Mus musculus  
DATE 20-Mar-1998  
ACCESSIONS S53028  
REFERENCES van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosten, J.; Jongen, W.A.; Bosch, D.; Stokman, W.J.; Ziegler, W.J.  
TITLE Subcloning and expression of antibody subunit genes yields high levels of functional antibodies in roots of transgenic tobacco.  
#status preliminary  
#accession S53028  
#molecule\_type mRNA

##molecule-type mRNA  
##accession D32513 #label VAN  
##cross-references DBM:J5318; NID:9523337  
##remarks heterotrimer: immunoglobulin  
##summary length 219 #molecular-weight 24049 #checksum 5937  
Query Match 13.1% Score 19; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 2,508-25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 100 LEIKADAPVGIIPPS 127  
QY 124 LEIKADAPVGIIPPS 142

RESULT 24  
ENTRY EKN518  
TITLE 19 kappa chain precursor V region (VNM178) - mouse  
ORIGIN 19 kappa chain precursor V region (VNM178) - mouse  
DATE 20-Mar-1998  
ACCESSION A01924  
REFERENCE 19 kappa chain precursor V region (VNM178) - mouse  
Cell (1980) 21:793-799  
#journal  
#title Variation in the crossover point of kappa immunoglobulin gene  
#cross-references DB:K00880; NID:9197443; PID:9197444  
#molecule-type DNA  
##accession A01924 #label MAX  
##cross-references DB:K00880; NID:9197443; PID:9197444  
##remarks the sequence was determined from the germline gene  
GENETICS 19/1  
COMPLEX 19/1  
No immunoglobulin heterotrimer antibody consists of two identical light (kappa or lambda) and two identical heavy (kappa or lambda) chains. The chains are held together by disulfide bonds, such as 19A and 19H, the subunits associate into larger oligomers. Immunoglobulin V region: immunoglobulin homology  
CLASSIFICATION heterotrimer  
FEATURE 1-22  
#domain signal sequence secretory predicted label 510V  
23-117  
#product 19 kappa chain V region (VNM178) status  
#molecule-type DNA  
#length 117 #molecular-weight 12954 #checksum 3822  
QY 124  
Query Match 12.4% Score 18; DB 1; Length 117;

organization and immunoglobulin genes encoding anti-DNA  
antibodies in lupus mice.  
##accession D32513  
##molecule-type DNA  
##cross-references DB:M20832; NID:9196941; PID:9196942  
##remarks heterotrimer: immunoglobulin  
##summary length 129 #molecular-weight 14097 #checksum 3457  
Query Match 11.7% Score 17; DB 2; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1,286-20;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 89 SCSDSLTISLSLEDP 105  
QY 87 SCSDSLTISLSLEDP 103

RESULT 27  
ENTRY E31720  
TITLE 19 kappa chain V region (9.42) - mouse  
ORIGIN 19 kappa chain V region (9.42) - mouse  
DATE 09-Mar-1990  
ACCESSION E31720  
REFERENCE 19 kappa chain V region (9.42) - mouse  
Proc. Natl. Acad. Sci. U.S.A. (1989) 86:6744-6747  
#journal  
#title Early rearrangements of genes encoding murine immunoglobulin  
#cross-references DB:M20832; NID:9196941; PID:9196942  
#molecule-type DNA  
##accession E31720 #label LAW  
##cross-references DB:M20832; NID:9196941; PID:9196942  
##remarks heterotrimer: immunoglobulin  
##summary length 94 #molecular-weight 1065 #checksum 2603  
Query Match 11.0% Score 16; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 2,616-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 DIOTGSPSSLSASLC 16  
QY 21 DIOTGSPSSLSASLC 36

Best Local Similarity 100.0%; Pred. No. 5,856-23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 21 RCDIOTGSPSSLSASLC 36  
QY 19 RCDIOTGSPSSLSASLC 36

RESULT 25  
ENTRY S40366  
TITLE 19 kappa chain V-J region - human  
ORIGIN 19 kappa chain V-J region - human  
DATE 10-Mar-1998  
ACCESSION S40366  
REFERENCE S40366  
#journal  
#title Expressed human immunoglobulin chi genes and their  
#cross-references DB:M20832; NID:9196941; PID:9196942  
#molecule-type mRNA  
##accession S40366 #label KLE  
##cross-references DB:M20832; NID:9196941; PID:9196942  
##remarks heterotrimer: immunoglobulin  
##summary length 107 #molecular-weight 11556 #checksum 3149  
Query Match 11.7% Score 17; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1,286-20;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 10 TRCDIOTGSPSSLSAS 26  
QY 18 TRCDIOTGSPSSLSAS 34

RESULT 26  
ENTRY D32513  
TITLE 19 kappa chain V region (clone 202.33) - mouse (fragment)  
ORIGIN 19 kappa chain V region (clone 202.33) - mouse (fragment)  
DATE 30-Sep-1993  
ACCESSION D32513  
REFERENCE D32513  
#journal  
#title 19 kappa chain V region (clone 202.33) - mouse (fragment)  
#cross-references DB:M20832; NID:9196941; PID:9196942  
#molecule-type DNA  
##accession D32513 #label TIL  
##cross-references DB:M20832; NID:9196941; PID:9196942  
##remarks heterotrimer: immunoglobulin  
##summary length 94 #molecular-weight 1065 #checksum 2603  
Query Match 11.0% Score 16; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 2,616-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 DIOTGSPSSLSASLC 16  
QY 21 DIOTGSPSSLSASLC 36

RESULT 29  
ENTRY PH1064  
TITLE 19 kappa chain V region (clone 202.54) - mouse (fragment)  
ORIGIN 19 kappa chain V region (clone 202.54) - mouse (fragment)  
DATE 15-Jun-1996  
ACCESSION PH1064  
REFERENCE PH1064  
#journal  
#title Both 19H and 19C anti-DNA antibodies are the products of  
#cross-references DB:M20832; NID:9196941; PID:9196942  
#molecule-type DNA  
##accession PH1064 #label TIL  
##cross-references DB:M20832; NID:9196941; PID:9196942  
##remarks heterotrimer: immunoglobulin  
##summary length 94 #molecular-weight 1065 #checksum 2603  
Query Match 11.0% Score 16; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 2,616-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 DIOTGSPSSLSASLC 16  
QY 21 DIOTGSPSSLSASLC 36

REMARKS Immunoglobulin  
SDMARKY length 97 checksum 1339

Query Match 11.0% Score 16; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

RESULT 30  
ENTRY 526332  
TITLE Ig kappa chain V region - mouse (fragment)  
ORIGINISM 19-Jan-1995  
DATE 19-Jan-1995  
ACCESSIONS 526332  
REFERENCES 526309  
\*authors Stark, S.E.; Caton, A.J.  
\*journal J. Exp. Med. (1991) 174:613-624  
\*note Anticodon change in a protein epitope use structurally distinct variable regions

accession 526332  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334064  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

accession 526331  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334064  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

CLASSIFICATION  
SDMARKY length 103 checksum 1197

Query Match 11.0% Score 16; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

Query Match 11.0% Score 16; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

RESULT 33  
ENTRY 526336  
TITLE Ig kappa chain V region (VH13) - mouse (fragment)  
ORIGINISM 08-Sep-1997  
DATE 08-Sep-1997  
ACCESSIONS 526336  
REFERENCES 526309  
\*authors Stark, S.E.; Caton, A.J.  
\*journal J. Exp. Med. (1991) 174:613-624  
\*note Anticodon change in a protein epitope use structurally distinct variable regions

accession 526336  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334064  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

CLASSIFICATION  
SDMARKY length 106 checksum 2278

Query Match 11.0% Score 16; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

RESULT 34  
ENTRY 526339  
TITLE Ig kappa chain V region (VH13) - mouse (fragment)  
ORIGINISM 15-Aug-1996  
DATE 15-Aug-1996  
ACCESSIONS 526339  
REFERENCES 526309  
\*authors Stark, S.E.; Caton, A.J.  
\*journal J. Exp. Med. (1991) 174:613-624  
\*note Anticodon change in a protein epitope use structurally distinct variable regions

accession 526339  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334064  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

CLASSIFICATION  
SDMARKY length 106 checksum 2278

Query Match 11.0% Score 16; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

ENTRY 526330  
TITLE Ig kappa chain V region - mouse  
ORIGINISM 13-Jan-1995  
DATE 13-Jan-1995  
ACCESSIONS 526330  
REFERENCES 526309  
\*authors Stark, S.E.; Caton, A.J.  
\*journal J. Exp. Med. (1991) 174:613-624  
\*note Anticodon change in a protein epitope use structurally distinct variable regions

accession 526330  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334063  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

CLASSIFICATION  
SDMARKY length 104 checksum 4741

Query Match 11.0% Score 16; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

RESULT 32  
ENTRY 526329  
TITLE Ig kappa chain V region - mouse  
ORIGINISM 13-Jan-1995  
DATE 13-Jan-1995  
ACCESSIONS 526329  
REFERENCES 526309  
\*authors Stark, S.E.; Caton, A.J.  
\*journal J. Exp. Med. (1991) 174:613-624  
\*note Anticodon change in a protein epitope use structurally distinct variable regions

accession 526329  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334059  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

CLASSIFICATION  
SDMARKY length 104 checksum 4817

Query Match 11.0% Score 16; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

Query Match 11.0% Score 16; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

RESULT 35  
ENTRY 526066  
TITLE Ig kappa chain V region (monoclonal antibody C3) - mouse  
ORIGINISM 23-Feb-1996  
DATE 23-Feb-1996  
ACCESSIONS 526066  
REFERENCES 526065  
\*authors Mison, M.W.; Pflanz, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogle, J.N.  
\*journal Nature Struct. Biol. (1995) 2:333-340  
\*note Anticodon change in a protein epitope use structurally distinct variable regions

accession 526066  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334063  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

CLASSIFICATION  
SDMARKY length 107 checksum 6711

Query Match 11.0% Score 16; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

RESULT 36  
ENTRY 526067  
TITLE Ig kappa chain V region (monoclonal antibody C3) - mouse  
ORIGINISM 23-Feb-1996  
DATE 23-Feb-1996  
ACCESSIONS 526067  
REFERENCES 526065  
\*authors Mison, M.W.; Pflanz, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogle, J.N.  
\*journal Nature Struct. Biol. (1995) 2:333-340  
\*note Anticodon change in a protein epitope use structurally distinct variable regions

accession 526067  
 \*\*molecule\_type mRNA  
 \*\*status preliminary  
 \*\*cross-references EMBL:552187; NID:952316; PID:9334063  
 #note the sequence of residues 1-6 and the corresponding nucleic acid sequence are not shown

CLASSIFICATION  
SDMARKY length 107 checksum 6711

Query Match 11.0% Score 16; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2,61e-18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 D10MT0SPSSLSASLG 16  
QY 21 D10MT0SPSSLSASLG 36

```

#author      Wren, M.W.; Hoegl, J.M.
#submitter   Submitted to the Brookhaven Protein Data Bank, January 1995
#date        19950116
#release     Yes
#comments    Contains X-ray crystallography, 3.0 angstroms, residues 1-227, 5'-23'-115
#citation     Superficially immunoglobulin V region: Immunoglobulin homology heterodimeric immunoglobulin
#keywords     IMMUNOGLOBULIN
#feature     FEATSTR
#misc       16-95
SUBNAM      23-93
            $domain immunoglobulin homology $label IMV
            $dufidid_bonds status experimental
            length 115 echnomax 7524

Query Match          11.0% Score 16; DB 2; Length 115;
                        Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matched             16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      100 PTRYGGCTGCTCAAGD 115
         |||||
OY      115 PTYGGCTGCTCAAGD 130

#type complete
A27594
Kappa chain precursor V-L1 region (Hala-6) - human
19-Nov-1989 Sequence_Revision 19-Nov-1989 seq-change
16-Aug-1996

A27594
Accessions
Author      Osterwey, S.J.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.;
            Schreiner, N.B.
Journal     J. Exp. Med. (1988) 167:488-501
Title       The kappa-deleting element: Germaline and rearranged,
            repressed references PMID:80184739
Accession   A27594
Status      not compared with conceptual translation
            $status-type DNA $label GAS
            $features
            $note      this sequence was translated from an aberrantly
                    rearranged kappa gene from lambda-producing B cells

GENETICS
Classification 2
$intmon      1971
Keywords     superfamily immunoglobulin V region: immunoglobulin homology
            heterodimeric: immunoglobulin
SUBNAM      $domain signal sequence status predicted $label SIC
            $length 116 molecular-weight 12739 echnomax 9571

Query Match          11.0% Score 16; DB 2; Length 116;

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      title
      The V(kappa) genes of the L regions and the repertoire of V
      kappa(108)p gene sequences in the human germ line.
**status
**molecule_type DNA
**preliminary
**cross_references EMBL:X7808; NID:9415363; PID:9415364
GENETICS
    siatrons
CLASSIFICATION
    /?+/-
    heterofamily immunoglobulin v region; immunoglobulin homology
    domain
SEQUENCE
    length 117 molecular_weight 12778 checksum 5619
Query Match
Best Local Similarity 100.0%; Pctd. No. 2.6E-18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          19 NCBI/JGSP/SPLS/AS 34
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[illegible]

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Db          21 RODIONTPSPSSLSMS 36
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Match Local Similarity 100.0% ; Pred. No. 2,61e-18;
Mismatches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          19 RODIONTPSPSSLSMS 34
|||||

RESULT      37
*****
ENTRY       B21056 #type fragment
TITLE       19 kappa chain precursor V-region (RH134) - human (fragment)
ORGANISM    03-Aug-1990 sequence_revision 03-Aug-1990 seqnt_change
DATE        20-Mar-1998
ACCESSIONS  B21056
REFERENCES  Bentley, D.L.; Rabbits, T.H.
            Cell (1989) 21,213-2189
            Evolution of immunoglobulin V genes: evidence indicating that
            by gene duplication human V-kappa sequences have diverged
            from conspecific mouse B319397.
            *cross-reference NIDB-B319397.
            accession B21056
            status preliminary
            submitter type 1-117 #label BMN
            #residues 19
CLASSIFICATION superfamily Immunoglobulin V region; immunoglobulin homology
            domain
            histocytamer; immunoglobulin
            length 117 technique 468

Query Match 11.0%; Score 16; Db 2; Length 117;
Match Local Similarity 100.0% ; Pred. No. 2,61e-18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          21 RODIONTPSPSSLSMS 36
|||||
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          19 RODIONTPSPSSLSMS 34
|||||

RESULT      38
*****
ENTRY       S41809 #type complete
TITLE       19 kappa chain precursor V-region A10 - human
ORGANISM    03-Sep-1995 sequence_revision 11-Jan-1995 seqnt_change
DATE        10-Sep-1997
ACCESSIONS  S41809
REFERENCES  Huber, C.; Schnabel, K.F.; Huber, E.; Klein, R.; Melnick, A.;
            Thibodeau, J.; Lamm, R.; Zachau, H.G.
            Eur. J. Immunol. (1989) 21,2865-2875
            authors

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QY	19	KC010H0TNPSS1281	34
RESULT	40	542263	*type complete
ENTRY		19	kappa chain v region (08) - human
TITLE		19	formal_name Homo sapiens common_name man
ORGANISM		19	08-sep-1993
DATE		542263	*sequence-revision 13-Jan-1995 text-change
ACCESSION		542263	
REFERENCE		542263	
AUTHORS		Socot, M.G.; Cushman, D.L.; McCourt, D.W.; Chung, C.; Nish, M.H.; K.T.; Thiele, R.; Quirel, E.K.; Zachau, H.G.;	
		*Journal (1993) 117:4007-4013	
*title		Clonal characterization of the human IgG antibody repertoire	
		1488 frequently expressed V <sub>H</sub> are heterogeneous.	
*accession		542263	
*status		Preliminary	
*status		sequence-type DNA 17 19101b1 SC0	
*sequence		*sequence-reference DBL:NC04855; NID:918593; PID:918594	
GENETICS		19/	
CLASSIFICATION		19/	
KEYWORDS		heterocistimer; immunoglobulin v region; immunoglobulin homology	
SIMILARITY		*length 117 *molecular-weight 12848 *checksum 7329	
Query Match		11 00; Score 16; DB 2; length 117;	
Best local similarity 100 00		0 0	
Matches	16;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	21	KC010H0TNPSS1281	36
QY	19	KC010H0TNPSS1281	34
ENTRY	41	521668	*type complete
TITLE		19	kappa chain v region (84) - human
ORGANISM		19	formal_name Homo sapiens common_name man
DATE		22-Nov-1993	*sequence-revision 10-Nov-1995 text-change
ACCESSION		521668	
REFERENCE		521668	
AUTHORS		Roeschenthaler, P.; Schaeble, K.F.; Thiele, R.; Zachau, H.G.;	
*Journal (1993) 117:177-186		08-sep-1993	
*title		Clonal characterization of the germline repertoire	
		of human immunoglobulin kappa genes.	
*sequence-reference NC0192816181			

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CLASSIFICATION      hyperfamily immunoglobulin V region: Immunoglobulin
REMARKS             heterotrimer: immunoglobulin
SUBUNIT            18kDa chain 902
Db                  21 RCDIOMGSPSSLAAS 36
Ov                  19 RCDIOMGSPSSLAAS 34
Quey Match          11.0%; Score 16; DB 2; Length 117;
                    Best Local Similarity 100.0%; Pval. No. 2.6E-18;
Matches            16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                    |||.....|||
ACCESSIONS          A01881; A1056
AUTHORS             Bentley, D.L.; Robbins, T.H.
JOURNAL             Nature (1980), 288: 73-73
TITLE               Two lambda-genes and a pseudogene.
SEQUENCE-REFERENCE  human immunoglobulin variable region genes - DNA sequences of
                    human V kappa genes and a pseudogene.
                    accession ID# 8109586
                    molecule-type DNA
                    reference 1-17 #label BEN
REFERENCE           A1055
                    authors Bentley, D.L.; Robbins, T.H.
                    journal Cell (1983) 32: 181-189
                    title   Recently duplicated human V kappa sequences have diverged
                    by gene conversion.
                    accession F01D:8112937
                    cross-references XRD:8112937
                    accession A1055
                    database-type NBR
GENETICS            CDB:ICENT1
                    gene     references CDB:13524
                    analysis 1971-79
                    introns 1971-79
COMPLEX             An immunoglobulin heterotrimeric subunit consists of two
                    identical light (lambda or lambda) and two identical heavy
                    chains. The heavy chain contains three interchain disulfide bonds. In some cases,
                    such as IgM and IgW, the subunits associate into larger
                    oligomers.

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Page 5

[illegible]

Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 24 RCDIOMTSPSSISLS 39  
CY 19 RCDIOMTSPSSISLS 34

RESULT 47  
ENTRY 540314 \*type complete  
TITLE 15 kappa chain V region: immunoglobulin homology  
ORGANISM Homo sapiens  
DATE 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 540312  
REFERENCE 540312  
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.  
#journal Eur. J. Immunol. (1993) 23:3248-3271  
#title Expressed human immunoglobulin chl genes and their  
#accession 540314  
#status preliminary; translation not shown  
#molecule\_type mRNA  
#cross-references EMBL:X7243  
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology  
REMARKS heterotrimer: immunoglobulin  
#length 124 #molecular\_weight 13196 #checksum 765  
Query Match 11.0% Score 16; DB 2; Length 123;  
Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 14 RCDIOMTSPSSISLS 29  
CY 19 RCDIOMTSPSSISLS 34

RESULT 48  
ENTRY 540331 \*type complete  
TITLE 19 kappa chain - human  
ORGANISM Homo sapiens  
DATE 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 540331  
REFERENCE 540331  
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.  
#journal Eur. J. Immunol. (1993) 23:3248-3271  
#title Expressed human immunoglobulin chl genes and their  
#accession 540331  
#status preliminary; translation not shown  
#molecule\_type mRNA  
#cross-references EMBL:X7243  
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology  
REMARKS heterotrimer: immunoglobulin  
#length 124 #molecular\_weight 13196 #checksum 765  
Query Match 11.0% Score 16; DB 2; Length 123;  
Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 14 RCDIOMTSPSSISLS 29  
CY 19 RCDIOMTSPSSISLS 34

ORGANISM Homo sapiens  
DATE 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 540331  
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#authors Klein, R.; Jaenichen, R.; Zachau, H.G.  
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#molecule\_type mRNA  
#cross-references EMBL:X7243  
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology  
REMARKS heterotrimer: immunoglobulin  
#length 124 #molecular\_weight 13196 #checksum 765  
Query Match 11.0% Score 16; DB 2; Length 123;  
Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 14 RCDIOMTSPSSISLS 29  
CY 19 RCDIOMTSPSSISLS 34

ORGANISM Homo sapiens  
DATE 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 540331  
REFERENCE 540331  
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.  
#journal Eur. J. Immunol. (1993) 23:3248-3271  
#title Expressed human immunoglobulin chl genes and their  
#accession 540331  
#status preliminary; translation not shown  
#molecule\_type mRNA  
#cross-references EMBL:X7243  
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology  
REMARKS heterotrimer: immunoglobulin  
#length 124 #molecular\_weight 13196 #checksum 765  
Query Match 11.0% Score 16; DB 2; Length 123;  
Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 14 RCDIOMTSPSSISLS 29  
CY 19 RCDIOMTSPSSISLS 34

Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 24 RCDIOMTSPSSISLS 39  
CY 19 RCDIOMTSPSSISLS 34

RESULT 47  
ENTRY 540314 \*type complete  
TITLE 15 kappa chain V region: immunoglobulin homology  
ORGANISM Homo sapiens  
DATE 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 540312  
REFERENCE 540312  
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.  
#journal Eur. J. Immunol. (1993) 23:3248-3271  
#title Expressed human immunoglobulin chl genes and their  
#accession 540314  
#status preliminary; translation not shown  
#molecule\_type mRNA  
#cross-references EMBL:X7243  
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology  
REMARKS heterotrimer: immunoglobulin  
#length 124 #molecular\_weight 13196 #checksum 765  
Query Match 11.0% Score 16; DB 2; Length 123;  
Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 14 RCDIOMTSPSSISLS 29  
CY 19 RCDIOMTSPSSISLS 34

RESULT 48  
ENTRY 540331 \*type complete  
TITLE 19 kappa chain - human  
ORGANISM Homo sapiens  
DATE 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change  
ACCESSIONS 540331  
REFERENCE 540331  
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.  
#journal Eur. J. Immunol. (1993) 23:3248-3271  
#title Expressed human immunoglobulin chl genes and their  
#accession 540331  
#status preliminary; translation not shown  
#molecule\_type mRNA  
#cross-references EMBL:X7243  
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology  
REMARKS heterotrimer: immunoglobulin  
#length 124 #molecular\_weight 13196 #checksum 765  
Query Match 11.0% Score 16; DB 2; Length 123;  
Best Local Similarity 100.0% Pred. No. 2 Size 10:  
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 14 RCDIOMTSPSSISLS 29  
CY 19 RCDIOMTSPSSISLS 34



!!SEQUENCE LIST 1.0  
(PEPTIDE) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-2 check: 4259 from: 1

FROMIG of: /home/obryen/ree455/olig/us08836455.pep  
sequence 2, application us/08836455

general information:  
applicant: chatterjee, malaya  
applicant: loon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: geneseqp: \* Sequences: 162,890 Total-length: 20,225,328 April 18, 1999 14:35

Database Release Information:  
Genesep-AA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

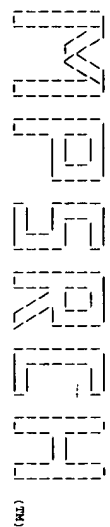
Word-size: 5 Words: 56705 Diagonals: 5,617 Total-diagonals: 43,681,344  
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 5.25

Sequence Strd Diag Score Width Documentation ..

GENESQ:W27119	+	0	145	1	Murine monoclonal anti-Idiotypic anti
GENESQ:P30251	+	2	129	1	Sequence of the leader, variable regi
GENESQ:R39569	+	113	100	1	Sequence of 520C9 sfv protein. New s
GENESQ:W02280	+	113	100	1	520C9 anti-c-erbB-2 two single chain
GENESQ:W80424	+	113	100	1	520C9 sfv sequence. Nucleic acid enc
GENESQ:W53170	+	113	100	1	520C9 anti-c-erbB-2 sfv' dimeric cons
GENESQ:W27121	+	404	94	1	Murine antibody light chain variable
GENESQ:R39571	+	404	94	1	Sequence of G-Fit. New single chain F
GENESQ:R21310	+	20	93	1	Light chain of Mif clone. Producing m
GENESQ:W18271	+	20	88	1	Prp 37 light chain variable region. N
GENESQ:W22537	+	2	85	1	Murine anti-human class II monoclonal
GENESQ:R79250	+	20	84	1	Light chain variable region for monoc
GENESQ:R79247	+	20	84	1	Light chain variable region for monoc
GENESQ:R78972	+	20	83	1	Light chain variable region for monoc
GENESQ:R52030	+	20	75	1	Light chain variable region of murine
GENESQ:W18270	+	20	71	1	Prp 28 light chain variable region. N
GENESQ:R21286	+	20	63	2	Murine VL kappa group V chain "a", sf
GENESQ:W18269	+	34	63	1	Prp 81 light chain variable region. N
GENESQ:W27089	+	20	60	1	Murine monoclonal antibody B9 light ch
GENESQ:W26728	+	0	56	1	Anti-Idiotypic antibody 3H1 light cha
GENESQ:R89686	+	0	56	1	Monoclonal anti-Idiotypic antibody 3H1
GENESQ:R88410	+	0	56	1	3H1 light chain variable region. Recd
GENESQ:R28670	+	0	54	1	PPM-X3 protein product. Reconstituted
GENESQ:R39265	+	20	54	1	Mouse C4G1 Ig light-chain. Compn. cc
GENESQ:W15935	+	20	54	1	Antibody 3G2 light chain variable reg
GENESQ:W49809	+	0	54	1	Variable region of mouse antibody C4G
GENESQ:W44123	+	20	53	1	Light chain variable region of human
GENESQ:W10233	+	0	53	1	TF8-5G9 CDR-grafted light chain. CDR-
GENESQ:R52040	+	20	53	1	Light chain variable region of murine
GENESQ:R15322	+	0	52	1	IL-2 chimeric antibody light chain. N
GENESQ:R84553	+	0	52	1	MAB SCH94.03 light chain. Monoclonal
GENESQ:W11918	+	0	52	1	Murine MAB SK48-F26 light chain. Recd
GENESQ:W70954	+	-33	52	3	Light chain of monoclonal antibody R5
GENESQ:R15321	+	0	51	1	IL-2 chimeric antibody light chain. N
GENESQ:R62881	+	0	50	1	Murine anti-human atherosclerotic pla
GENESQ:R09426	+	0	49	1	ME4 Light Chain V region (mouse). Ch1
GENESQ:R32121	+	0	49	1	Anti-CD4 antibody M7 15.1 light chain
GENESQ:W06215	+	0	49	1	MAB ME4 light chain variable region.
GENESQ:R29010	+	0	48	1	p146-K3 protein product. Reconstitute
GENESQ:W16620	+	20	47	1	Anti-human FasL antibody (NOK1) light
GENESQ:W11815	+	20	47	1	Mouse anti-human Fas ligand antibody
GENESQ:W04177	+	0	47	1	Variant variable light chain of Fas l
GENESQ:W60033	+	0	47	1	Mouse antibody F919-9-18 light chain
GENESQ:R53803	+	-21	46	2	FAB light chain for F19.9. New ligand
GENESQ:W35125	+	-20	46	1	R. piplens recombinant RNase ronc fus
GENESQ:W35130	+	-20	46	1	R. piplens recombinant RNase ronc fus
GENESQ:W35129	+	-20	46	1	R. piplens recombinant RNase ronc fus
GENESQ:W35127	+	-20	46	1	R. piplens recombinant RNase ronc fus
GENESQ:W35126	+	122	46	1	R. piplens recombinant RNase ronc fus
GENESQ:W35128	+	100	46	1	R. piplens recombinant RNase ronc fus

# of diag. containing matches at least 5 amino acids long

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PT Company, cancer antigen-targeting antibody fragment constructs  
 CC Example 1: Column 33-36, 30pp: English  
 CC Variable heavy (VH) and variable light (VL) genes were cloned from  
 CC a 5209 hybridoma cDNA library, using probes directed toward the  
 CC heavy chain (HC) and light chain (LC) regions, respectively. The  
 CC gene was constructed by connecting the VH and VL genes, and  
 CC ser rich polypeptide linker. The resulting 5209 two apt gene,  
 CC which encodes the present sequence, was inserted into an expression  
 CC vector, and the culture medium was collected, and protein expression induced by  
 CC the addition of IPTG to the culture medium.  
 CC A c-myc protein product, and the 2 apt protein prod. can be  
 CC used for in vivo imaging, and drug targeting experiments. The  
 CC apt protein product is a homodimer, in which both fragments target  
 CC the same antigen. The apt protein product is also used for antigen  
 CC prod. fragments.  
 CC Sequence 243 AA.

Query Match 20.0% Score 29; DB 18; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 aptfgrgsdyslttslsedrv 217  
 |||||  
 76 SCVPRFSGSDYSLTSLSEEDRV 104

Query Match 20.0% Score 29; DB 18; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 aptfgrgsdyslttslsedrv 217  
 |||||  
 76 SCVPRFSGSDYSLTSLSEEDRV 104

RESULT 8  
 ID R39569 standard; Protein: 246 AA.  
 AC R39569;  
 DE 07-FEB-1994 (first entry)  
 KW Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;  
 KW bioengineered single polypeptide chain binding site; aa.  
 OS Synthetic.  
 PD 19-AUG-1993;  
 PR 05-FEB-1993; 001055;  
 PA (CENTU) CENTU ONCOLOGY CORP.  
 PI Houston TX, Huston JS, Oppermann H, Ring DB;  
 WP1: 93-27288/34.  
 DR N-PSDB: Q46084.  
 PT Antigen binding; C-erbB-2 binding to C-erbB-2 tumour  
 PT antigen; for imaging or treating breast or ovarian cancer etc.  
 CC Claim 4; pages 60-61; 87pp; English.  
 CC C-erbB-2 refers to a protein antigen expressed on the surface of  
 CC tumour cells, such as breast and ovarian tumour cells, which is an  
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric

Query Match 20.0% Score 29; DB 18; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 aptfgrgsdyslttslsedrv 217  
 |||||  
 76 SCVPRFSGSDYSLTSLSEEDRV 104

Query Match 20.0% Score 29; DB 18; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 aptfgrgsdyslttslsedrv 217  
 |||||  
 76 SCVPRFSGSDYSLTSLSEEDRV 104

RESULT 10  
 ID P93035 standard; Protein: 213 AA.  
 AC P93035;  
 DE 14-MAR-1990 (first entry)  
 KW Chimeric antibody light chain variable region;  
 KW human; chimeric antibody; light chain variable region.  
 OS Mos.  
 PD 25-APR-1989;  
 PR 15-APR-1989; 303814;  
 PA (EliL) Eli Lilly and Co.  
 PI Beavers LS, Bumol TF, Gadski RA, Weigel BJ;  
 DR N-PSDB: 89-11203/43.  
 PT Recombinant DNA cDNA, producing antibodies - monoclonal and  
 PT chimeric derived from monoclonal antibody K5/4.  
 CC Claim 1; page 49; 89pp; English.  
 CC The sequence encodes the light chain of Mab K5/4, used to  
 CC produce a chimeric antibody K5/4, which is a murine antibody  
 CC which binds to surface antigens on tumour cells. The use of  
 CC human C regions avoids immunological problems during treatment.  
 CC Sequence 213 AA.

Query Match 19.3% Score 28; DB 1; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.98e-24;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 94 pttgggkrlkrlkdaapvslfppas 121  
 |||||  
 115 pttgggkrlkrlkdaapvslfppas 142

RESULT 11  
 ID W27089 standard; Protein: 214 AA.  
 AC W27089;  
 DE 18-NOV-1997 (first entry)  
 KW House monoclonal antibody B9 light chain;  
 KW house monoclonal antibody B-100; antitumor necrosis factor protein;  
 KW antibody; B9.  
 OS Mus musculus.  
 PD 24-34;  
 PR 17-MAR-1995; 300462;  
 PA (PROT-) PROTEIN ENG RES INST.  
 PI WPI: 96-44329/44.  
 DR N-PSDB: T87818.  
 PT region /Label= CDR3

CC pt. of about 5.3 (see Q46083, R39568). A single chain Fv (scFv)  
 CC is a covalently linked VH-VL heterodimer which is expressed from  
 CC a gene construct including VH- and VL-encoding genes connected by  
 CC a linker sequence. The scFv is produced by recombinant DNA tech-  
 CC niques. The scFv is used for imaging or treating breast or ovarian cancer etc.  
 CC AA residues 116-135 in R39569 which include the C-terminus of the  
 CC linker sequence in R39572. Using Q46084 for the 5209 monoclonal  
 CC antibody, a single chain polypeptide can be produced having a  
 CC sequence of about 5.3 (see Q46083, R39568).  
 CC refers to the location of a stop codon in Q46084.

Query Match 20.0% Score 29; DB 8; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 aptfgrgsdyslttslsedrv 217  
 |||||  
 76 SCVPRFSGSDYSLTSLSEEDRV 104

Query Match 20.0% Score 29; DB 8; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 aptfgrgsdyslttslsedrv 217  
 |||||  
 76 SCVPRFSGSDYSLTSLSEEDRV 104

RESULT 9  
 ID R39572 standard; Protein: 534 AA.  
 AC R39572;  
 DE 07-FEB-1994 (first entry)  
 KW Sequence of C-erbB-2; C-PTT.  
 OS Synthetic; C-erbB-2; C-PTT.  
 PD 19-AUG-1993;  
 PR 05-FEB-1993; 001055;  
 PA (CENTU) CENTU ONCOLOGY CORP.  
 PI Houston TX, Huston JS, Oppermann H, Ring DB;  
 WP1: 93-27288/34.  
 DR N-PSDB: Q46084.  
 PT New single chain Fv polypeptide binding to C-erbB-2 tumour  
 PT antigen; for imaging or treating breast or ovarian cancer etc.  
 CC Example; pages 65-68; 87pp; English.  
 CC C-erbB-2 refers to a protein antigen expressed on the surface of  
 CC tumour cells, such as breast and ovarian tumour cells, which is an  
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric  
 CC pt. of about 5.3 (see Q46083, R39568).  
 CC Sequence 534 AA.

Query Match 20.0% Score 29; DB 8; Length 534;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 480 aptfgrgsdyslttslsedrv 508  
 |||||  
 108-214  
 /Label= C-PTT

Query Match 20.0% Score 29; DB 8; Length 534;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 480 aptfgrgsdyslttslsedrv 508  
 |||||  
 108-214  
 /Label= C-PTT

Query Match 20.0% Score 29; DB 8; Length 534;  
 Best Local Similarity 100.0%; Pred. No. 9,98e-26;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 480 aptfgrgsdyslttslsedrv 508  
 |||||  
 108-214  
 /Label= C-PTT

RESULT 12  
 ID W19935 standard; Protein: 216 AA.  
 AC W19935;  
 DE 09-DEC-1997 (first entry)  
 KW Antibody 302 light chain variable region;  
 KW catalytic antibody; antitumor necrosis factor; hydrazide;  
 KW NAA302; NAA302; ds.  
 OS misc.  
 PD 24-34;  
 PR 17-MAR-1995; 300462;  
 PA (PROT-) PROTEIN ENG RES INST.  
 PI WPI: 96-44329/44.  
 DR N-PSDB: T87818.  
 PT region /Label= CDR3

PT Catelect antibody for antineoplastic hydrolysis of amino acid  
PS ester. also new hybridoma secreting the antibody  
PS Disclousure: Page 39: 1999: Japanese.  
CC The present disclosure describes new catalytic antibodies which hydrolyze amino  
CC acid esters and amide bonds. Preferably the ester, amide, or  
CC amide bonds are hydrolyzed. The antibodies are generated from an  
CC immunoscreened animal. The antibody is generated by PCR amplifying the  
CC variable regions derived from a repertoire of antibodies from an  
CC immunoscreened animal. The variable regions, esp the complementarity determining  
CC regions (CDR, see R5462-93 for examples of CDRs) from the immunotolerant  
CC animal, antibodies are used to construct an antibody against a target  
CC antigen. The antibodies generated can be used in the diagnosis, e.g.  
CC detection of the immunoreactive antigen, or in therapy, e.g. of cancer.  
CC The antibodies generated can be used in the diagnosis, e.g. of cancer.  
CC Production of the antibody allows rapid and sensitive isolation of  
CC antibodies that would be difficult to isolate by standard methods. The  
CC antibodies produced have greater binding affinity than those produced by  
CC conventional hybridoma methods.  
CC Sequence 216 AA:  
50  
Query Match 19.3% Score 28: DB 15: Length 216:  
Best Local Similarity 100.0%: Pred. No. 1.99e-24:  
Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 95 PYTGCGTATKTRKADAPVATLPPAS 132  
QY 115 PYTGCGTATKTRKADAPVATLPPAS 142  
|||||  
RESULT 13  
ID R5459 standard: Protein: 218 AA.  
AC R5459:  
DE 07-FEB-1996 (first entry)  
DT Mouse antibody F33-2 light chain variable region protein sequence.  
PR Primer: amplification: PCR: mouse: kappa chain: heavy chain: Fab:  
KW antibody: immunoreactive: animal: variegated display library: foetal:  
KW variable region: antigen: immunoreactive: cell surface marker: foetal:  
KW cancer: stem cell: variant: therapy: Alzheimer's disease: hybridoma:  
KW familial hypercholesterolemia: binding affinity.  
PS M09515982.42.  
PD 15-JUN-1995.  
PF 08-DEC-1994: D51406.  
PR 08-DEC-1994: D51406.  
PR 08-DEC-1994: D51406.  
PA (GENE) GENZYME CORP.  
PI Baramian G, Copeland DP, Hillhouse D, Johnson T:  
DR R-5459: 092501. Antibodies specific for immunoreactive epitopes  
DR generated by selection from variegated V gene library cloned from  
PT Immunotolerance derived antibody repertoire, useful in diagnosis,  
PT putien, and therapy, e.g. of cancer

PT Immunotolerance derived antibody repertoire, useful in diagnosis,  
PS Disclousure: Page 39: 1999: English.  
CC The sequence of the light chain variable region from the mouse antibody  
CC F33-2 is disclosed. The sequence is generated by PCR amplifying the  
CC variable regions derived from a repertoire of antibodies from an  
CC immunoscreened animal. The variable regions, esp the complementarity determining  
CC regions (CDR, see R5462-93 for examples of CDRs) from the immunotolerant  
CC animal, antibodies are used to construct an antibody against a target  
CC antigen. The antibodies generated can be used in the diagnosis, e.g.  
CC detection of the immunoreactive antigen, or in therapy, e.g. of cancer.  
CC The antibodies generated can be used in the diagnosis, e.g. of cancer.  
CC Production of the antibody allows rapid and sensitive isolation of  
CC antibodies that would be difficult to isolate by standard methods. The  
CC antibodies produced have greater binding affinity than those produced by  
CC conventional hybridoma methods.  
CC Sequence 218 AA:  
50  
Query Match 19.3% Score 28: DB 15: Length 218:  
Best Local Similarity 100.0%: Pred. No. 1.99e-24:  
Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 95 PYTGCGTATKTRKADAPVATLPPAS 132  
QY 115 PYTGCGTATKTRKADAPVATLPPAS 142  
|||||  
RESULT 15  
ID R5443 standard: Protein: 240 AA.  
AC R5443:  
DE 07-FEB-1996 (first entry)  
DT Single chain Fv from pscv1 for blocking HIV binding to ICAM-1.  
PR antigen-binding fragment: inflammation: auto-immune disease.  
KW Mono antigen.  
PS M09515982.42.  
PD 15-JUN-1995.  
PF 01-JUN-1990: D513001.  
PR 01-JUN-1990: D513001.  
PR 01-JUN-1990: D513001.  
PA (GENE) GENZYME CORP.  
PI Baramian G, Copeland DP, Hillhouse D, Johnson T:  
DR R-5443: 092501. Antibodies specific for immunoreactive epitopes  
DR generated by selection from variegated V gene library cloned from  
PT Immunotolerance derived antibody repertoire, useful in diagnosis,  
PT putien, and therapy, e.g. of cancer

PS Disclousure: Page 39: 1999: English.  
CC The sequence of the light chain variable region from the mouse antibody  
CC F33-2 is disclosed. The sequence is generated by PCR amplifying the  
CC variable regions derived from a repertoire of antibodies from an  
CC immunoscreened animal. The variable regions, esp the complementarity determining  
CC regions (CDR, see R5462-93 for examples of CDRs) from the immunotolerant  
CC animal, antibodies are used to construct an antibody against a target  
CC antigen. The antibodies generated can be used in the diagnosis, e.g.  
CC detection of the immunoreactive antigen, or in therapy, e.g. of cancer.  
CC The antibodies generated can be used in the diagnosis, e.g. of cancer.  
CC Production of the antibody allows rapid and sensitive isolation of  
CC antibodies that would be difficult to isolate by standard methods. The  
CC antibodies produced have greater binding affinity than those produced by  
CC conventional hybridoma methods.  
CC Sequence 218 AA:  
50  
Query Match 19.3% Score 28: DB 15: Length 218:  
Best Local Similarity 100.0%: Pred. No. 1.99e-24:  
Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 95 PYTGCGTATKTRKADAPVATLPPAS 132  
QY 115 PYTGCGTATKTRKADAPVATLPPAS 142  
|||||  
RESULT 14  
ID R5459 standard: Protein: 218 AA.  
AC R5459:  
DE 07-FEB-1996 (first entry)  
DT Mouse antibody F33-2 light chain variable region protein sequence.  
PR Primer: amplification: PCR: mouse: kappa chain: heavy chain: Fab:  
KW antibody: immunoreactive: animal: variegated display library: foetal:  
KW variable region: antigen: immunoreactive: cell surface marker: foetal:  
KW cancer: stem cell: variant: therapy: Alzheimer's disease: hybridoma:  
KW familial hypercholesterolemia: binding affinity.  
PS M09515982.42.  
PD 15-JUN-1995.  
PF 08-DEC-1994: D51406.  
PR 08-DEC-1994: D51406.  
PR 08-DEC-1994: D51406.  
PA (GENE) GENZYME CORP.  
PI Baramian G, Copeland DP, Hillhouse D, Johnson T:  
DR R-5459: 092501. Antibodies specific for immunoreactive epitopes  
DR generated by selection from variegated V gene library cloned from  
PT Immunotolerance derived antibody repertoire, useful in diagnosis,  
PT putien, and therapy, e.g. of cancer

CC which included a Gly-Gly-Gly-Gly-Gly-Gly linker between the L  
CC and H chains. The sequence is generated by PCR amplifying the  
CC variable regions derived from a repertoire of antibodies from an  
CC immunoscreened animal. The variable regions, esp the complementarity determining  
CC regions (CDR, see R5462-93 for examples of CDRs) from the immunotolerant  
CC animal, antibodies are used to construct an antibody against a target  
CC antigen. The antibodies generated can be used in the diagnosis, e.g.  
CC detection of the immunoreactive antigen, or in therapy, e.g. of cancer.  
CC The antibodies generated can be used in the diagnosis, e.g. of cancer.  
CC Production of the antibody allows rapid and sensitive isolation of  
CC antibodies that would be difficult to isolate by standard methods. The  
CC antibodies produced have greater binding affinity than those produced by  
CC conventional hybridoma methods.  
CC Sequence 240 AA:  
50  
Query Match 19.3% Score 28: DB 15: Length 240:  
Best Local Similarity 100.0%: Pred. No. 1.99e-24:  
Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 95 PYTGCGTATKTRKADAPVATLPPAS 132  
QY 115 PYTGCGTATKTRKADAPVATLPPAS 142  
|||||  
RESULT 16  
ID R5459 standard: peptide: 109 AA.  
AC R5459:  
DE 07-FEB-1996 (first entry)  
DT PrP 37 light chain variable region.  
PR PrP 37 light chain variable region.  
KW Prion protein: PrP: heavy chain variable region: antibody: scrapie:  
KW central nervous system spongiform encephalopathy: human: therapy:  
KW transmissible neurodegenerative disease: Creutzfeldt-Jakob Disease:  
KW bovine spongiform encephalopathy: feline spongiform encephalopathy:  
KW BSE: Creutzfeldt-Jakob Disease.  
PS M09515982.42.  
PD 15-JUN-1995.  
PF 01-JUN-1990: D513001.  
PR 01-JUN-1990: D513001.  
PR 01-JUN-1990: D513001.  
PA (GENE) GENZYME CORP.  
PI Baramian G, Copeland DP, Hillhouse D, Johnson T:  
DR R-5459: 092501. Antibodies specific for immunoreactive epitopes  
DR generated by selection from variegated V gene library cloned from  
PT Immunotolerance derived antibody repertoire, useful in diagnosis,  
PT putien, and therapy, e.g. of cancer









Db 118 f5g9g7k4t9zdeevys10fpa5 143  
 0Y 117 f5e0g7k4t9zdeevys10fpa5 142

AC	RESIDUE	standard; Protein; 239 AA.
AD	R76087	
AE	R76087	21-NOV-1995 (first entry)
AF	MA 55.1.1	118nt chain.
AG	MA 55.1.1	118nt chain.
AH	CA5.5	containing structure complementary determining region; CDR
AI	CA5.5	containing structure complementary determining region; CDR
AJ	monoclonal antibody; MAb; immunoreacted antigen; hybridoma;	
AK	transgenic animal; transgenic plant; antibody engineering;	
AL	humanized antibody; immunotoxin.	
AM	MA 55.1.1	
AN	Key word	Location/Qualifiers
AO	peptide	1..20
AP	peptide	21..200
AQ	protein	1..200
AR	protein	1..200
AS	protein	1..200
AT	protein	1..200
AV	protein	1..200
AW	protein	1..200
AX	protein	1..200
AY	protein	1..200
AZ	protein	1..200
BA	protein	1..200
BB	protein	1..200
BC	protein	1..200
BD	protein	1..200
BE	protein	1..200
BF	protein	1..200
BG	protein	1..200
BH	protein	1..200
BI	protein	1..200
BJ	protein	1..200
BK	protein	1..200
BL	protein	1..200
BM	protein	1..200
BN	protein	1..200
BO	protein	1..200
BP	protein	1..200
BQ	protein	1..200
BR	protein	1..200
BS	protein	1..200
BT	protein	1..200
BV	protein	1..200
BW	protein	1..200
BX	protein	1..200
BY	protein	1..200
BZ	protein	1..200
CA	protein	1..200
CB	protein	1..200
CC	protein	1..200
CD	protein	1..200
CE	protein	1..200
CF	protein	1..200
CG	protein	1..200
CH	protein	1..200
CI	protein	1..200
CJ	protein	1..200
CK	protein	1..200
CL	protein	1..200
CM	protein	1..200
CN	protein	1..200
CO	protein	1..200
CP	protein	1..200
CQ	protein	1..200
CR	protein	1..200
CS	protein	1..200
CT	protein	1..200
CU	protein	1..200
CV	protein	1..200
CW	protein	1..200
CX	protein	1..200
CY	protein	1..200
CA	protein	1..200
CB	protein	1..200
CC	protein	1..200
CD	protein	1..200
CE	protein	1..200
CF	protein	1..200
CG	protein	1..200
CH	protein	1..200
CI	protein	1..200
CJ	protein	1..200
CK	protein	1..200
CL	protein	1..200
CM	protein	1..200
CN	protein	1..200
CO	protein	1..200
CP	protein	1..200
CQ	protein	1..200
CR	protein	1..200
CS	protein	1..200
CT	protein	1..200
CU	protein	1..200
CV	protein	1..200
CW	protein	1..200
CX	protein	1..200
CY	protein	1..200
CA	protein	1..200
CB	protein	1..200
CC	protein	1..200
CD	protein	1..200
CE	protein	1..200
CF	protein	1..200
CG	protein	1..200
CH	protein	1..200
CI	protein	1..200
CJ	protein	1..200
CK	protein	1..200
CL	protein	1..200
CM	protein	1..200
CN	protein	1..200
CO	protein	1..200
CP	protein	1..200
CQ	protein	1..200
CR	protein	1..200
CS	protein	1..200
CT	protein	1..200
CU	protein	1..200
CV	protein	1..200
CW	protein	1..200
CX	protein	1..200
CY	protein	1..200
CA	protein	1..200
CB	protein	1..200
CC	protein	1..200
CD	protein	1..200
CE	protein	1..200
CF	protein	1..200
CG	protein	1..200
CH	protein	1..200
CI	protein	1..200
CJ	protein	1..200
CK	protein	1..200
CL	protein	1..200
CM	protein	1..200
CN	protein	1..200
CO	protein	1..200
CP	protein	1..200
CQ	protein	1..200
CR	protein	1..200
CS	protein	1..200
CT	protein	1..200
CU	protein	1..200

[illegible]

Dh	122	tggagatcctacataagaatgaaatgaagaa	0	Mismatches	0	Indels	0	Gaps	0
Oy	117	ttgcgtcttcttccadgaatttccttgcctg	142						

RESULT 35  
ID WJ121 standard; Protein: 107 AA

AC	W27121:	
AD	04-JAN-1998 (first entry)	
AF	anti-idiotypic light chain variable region consensus.	
AG	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
AM	human milk fat globulin (MFG) tumor; breast cancer; vaccine.	
AN	human milk fat globulin (MFG) tumor; breast cancer; vaccine.	
AO	Mus masculinus.	
AP	Key	Location/Qualifiers
AQ	Region	11b1a1 - CD31
AR	Region	/note= "complementarily determining region 1"
AS	Region	11b1a1 - CD32
AT	Region	/note= "complementarily determining region 2"
AV	Region	68_96
AW	Region	11b1a1 - CD33
AX	Region	/note= "complementarily determining region 3"
AY	06-07-2006-942	
AZ	26-JUN-1997	
BA	19-DEC-1996: D20757.	
BB	19-DEC-1996: D20757.	
BC	19-DEC-1996: D20757.	
BD	20-DEC-1996: D20757.	
BE	26-JAN-1996: D20757.	
BF	26-JAN-1996: D20757.	
BG	(RENT) DMTV-ENZYCLIS.	
BH	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BI	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BJ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BK	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BL	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BM	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BN	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BO	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BP	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BQ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BR	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BS	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BT	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BV	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BW	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BX	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BY	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
BZ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CA	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CB	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CC	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CD	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CE	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CF	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CG	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CH	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CI	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CJ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CK	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CL	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CM	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CN	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CO	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CP	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CQ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CR	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CS	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CT	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CU	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CV	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CW	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CX	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CY	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
CZ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DA	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DB	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DC	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DD	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DE	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DF	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DG	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DH	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DI	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DJ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DK	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DL	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DM	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DN	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DO	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DP	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DQ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DR	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DS	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DT	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DU	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DV	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DW	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DX	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DY	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
DZ	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EA	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EB	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EC	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
ED	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EE	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EF	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EG	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EH	Monoclonal antibody 11D10 anti-idiotypic antibody; mucln:	
EI	Monoc	

Db 118 149ggttcttctatctatgacatctctgctgagaa 142

```
Query Match      17.2%   Score 25    DB 35    length 107
Best Local Similarity 100.0%   Pred. No. 1,48-20;
Matches          25    Conservative 0    Mismatches 0    Indels 0    Gaps 0
DB              56    aggttttggagtgatgattatlas 80
                | | | | | | | | | | | | | | | | | | | | | | | |
QY              76    scppmmscscscscscscscscscscscscs 100
```

CY	118	FOCOTETRIEINOMAPVTSIPSSPS	142
RESULT	37		
AD	89466	standard: Protein: 142 MA.	
AD	89466		
DT	11-OCT-1986	(first entry)	
DT	11-OCT-1986		
RE	Monoclonal anti-dsFp antibody 3H1 light chain variable region.		
RE	carcinoembryonic antigen: monoclonal antibody: CEA.		
KW	vaccine: immunotherapy: tumor associated antigen: cancer:		





41. R3720 standard: peptide: 153 Aa.  
 ID R3720  
 DT 23-MOV-1995 (first entry)  
 DE Mouse monoclonal antibody 1668 light chain sequence derived from  
 DB cDNA.  
 OS Synthetic.  
 MO M0916038-A.  
 PR 15-MOV-1995.  
 PA 06-MOV-1994.  
 PA (MERC)/ MENCER C P  
 PA (TCEL-) T CELL SCI INC.  
 DE Lm AY.  
 DE Lm AY.  
 DE Lm AY.  
 PR Human 15-241327/29.  
 PT Useful for treatment of Crohn's disease and Multiple Sclerosis  
 PS Discovered: Page 63: 92pp: English.  
 CS A mouse monoclonal antibody (mab), 1668, which recognizes human V  
 CC framework chain humanized by CDR grafting certain CDR and select  
 CC REI light chain frameworks. The mab binds into CDR heavy chain and  
 CC heavy (19g1) and light (k) chains in mammalian cell expression  
 CC vectors V16H Neo and DHFR selection markers, respectively, were  
 CC followed by an auto- and DHFR- Chinese hamster fibroblast (CHO) cell line  
 CC selected and designated "TM29" application. The humanized Mab that was  
 CC TCR V beta 8.1. It is used as a therapeutic agent for  
 CC Crohn's disease.  
 CC Sequence: 153 Aa.  
 Query Match 15.24; Score 23; DB 11; Length 153;  
 Match Local Similarity 100.00; Pred. No. 9.52e-11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps  
 Db 133 gtrk1c1xkdaapvfwfss 153  
 ||||||||||||||||||||  
 121 GTRK1C1XKDAAPVFWWFSS 142  
 C7  
 RESULT 42  
 ID R3802 standard: Protein: 220 Aa.  
 DE R3802-1996 (first entry)  
 DE PAD light chain for JMCY  
 NM MNC6003: V-mu1; synthetic; E. coli; protease inhibitor; treatment  
 NM of intestinal variable domain; framework region; beta-barrel;  
 NM beta-sheet; Another complementarily determining regions; redolosing

[illegible][illegible]

PR 07-MAY-1993; JP-13108.  
PA (NIRS) JAPAN TOBACCO INC.  
DR KUREHA PHARMACEUTICAL CO. LTD.  
NM N-PSDB: Q79929.  
CC  
PT tobacco plants producing anti-tobacco mosaic virus  
TS esp. tobacco plants producing anti-tobacco mosaic virus  
CC Example 21 antibody p14, 36pp; Japanese  
CC 079929 and 079930 encode 866757 and 866758, the light and heavy  
CC chains of an animal derived anti-tobacco mosaic virus (TMV)  
CC monoclonal antibody. The cDNA was incorporated into a T1  
CC plasmid vector and transformed into E. coli.  
CC The resultant plant expressed TMV resistant tobacco plants.  
CC tobacco plants, making them TMV resistant to the plant transformation  
CC also be biotransformed for the prodn. of anti-virus antibodies  
SC sequence 359 NA.

Query Match 15.28; Score 23; DB 8; Length 239;  
Best Local Similarity 100.0%; Pred. No. 9,52e+17;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 126 gtblxleakadapvslipss 147  
Gy 121 GTTLEKRDNAAPVTSLIPSS 142

RESULT 44  
ID R39573 standard; Protein: 667 NA.  
AC R39573 standard; Protein: 667 NA.  
DE 07-FEB-1994 (first entry)  
DE Sequence of 741 bp-PD10  
NM Single chain Fv polypeptide; VH-VL heterodimer; Immunoglobulin Ig:  
OS Pseudomona  
PN MO3918185-A.  
PD 18-MAR-1993; DB1055  
PD 06-FEB-1993; DB1055  
PR 06-FEB-1993; DB1055  
PA (CETU) Cetus Oncology Corp.  
PA (CRNA-) CHEVATIVE BIOMOLECULES INC.  
DR Houston TX; Ruston JS; Oppermann H; Ring DB;  
DR N-PDSB: Q46088/34.

PT New single chain Fv polypeptide binding to C-erbB-2 tumour  
PT antigen - for tagging or treating breast or ovarian cancer etc.  
CC C-erbB-2 protein 1.7-4.8 kDa; English. expressed on the surface of  
CC tumour cells, such as breast and ovarian carcinomas.  
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric

CC pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sFv)  
CC is covalently linked to a pseudomonas toxin which is expressed from  
CC a gene fusion including VH- and VL regions. The linker sequences are  
CC a peptide encoding linker. Such linker sequences are set forth in  
CC literature 116-115 in R39569, which includes parts of the 16 AA  
CC linkers at amino acids 372-382. Using Q46084 for the 520c9 monoclonal  
CC antibody a single chain sFv. Owing to the presence of a cysteine  
CC binding affinity for a C-erbB-2 related antigen produced having a strong  
CC the pseudomonal exotoxin fragment analogous to ricin A chain, PD10,  
CC the resulting library contains remnants of the anti-C-erbB-2 Fv  
CC protein, which was constructed with the 16 AA linker between the  
CC chain initially was left on the protein. X in R39573 refers to  
CC penm. of stop codon in cDNA.  
SC sequence 667 NA.

Query Match 15.28; Score 23; DB 8; Length 667;  
Best Local Similarity 100.0%; Pred. No. 9,52e+17;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 236 gtblxleakadapvslipss 257  
Gy 121 GTTLEKRDNAAPVTSLIPSS 142

RESULT 45  
ID R15440 standard; Protein: 125 NA.  
AC R15440 standard; Protein: 125 NA.  
DE 25-FEB-1992 (first entry)  
DE Light chain variable region of Mab 2C2.  
NM RHV; IGM-1; antigen-binding fragment; inflammation;  
NM RHV; IGM-1; antigen-binding fragment; inflammation;  
OS Homo sapiens  
PN EP-459377-A.  
PD 04-DEC-1991; DB10143  
PD 25-FEB-1992; DB10143  
PR 01-JUN-1990; DB101001  
PA (MERI) MERCK & CO INC.  
PI Colomo RJ; Cordia JR; Tomasini JE; Sarda WV;  
PT Microbial antigens and polymers of monoclonal antibody - can block  
PT attachment of rhinovirus ligands to inter-cellular adhesion  
PT molecule (ICAM-1) Page 20; 36pp; English  
CC claim 1: Page 20; 36pp; English  
CC 1 of 10M-1. One peptide fragments from Mab's specific for domain  
CC rhinovirus infection. See R15437-R15443.  
SC sequence 125 NA.

Query Match 14.58; Score 21; DB 3; Length 125;  
Best Local Similarity 100.0%; Pred. No. 1,72e+16;

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 105 gttctctatadpvtatp 145  
121 CITEIRDAAPVPSIPPS 141

Query 46  
105 gttctctatadpvtatp 145  
121 CITEIRDAAPVPSIPPS 141

RESULT 46  
ID: 14576 standard: Protein: 147 AA.  
DE: 10-JUN-1997 (first entry)  
DE: Mouse anti-idiotypic antibody 1598 light chain variable region.  
DE: Anti-idiotypic; anti-EGFR; epidermal growth factor receptor; tumour;  
DE: cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacturer; 86.  
DE: Key molecule.  
PE: Location/Qualifiers  
FT peptide 1..24  
FT /label= sig\_peptide  
FT region 25..47  
FT /label= FR1  
FT region 48..58  
FT /note= "framework region 1"  
FT region 59..71  
FT /note= "complementarity determining region 1"  
FT region 72..84  
FT /label= FR2  
FT region 85..97  
FT /note= "framework region 2"  
FT region 98..110  
FT /label= CDR3  
FT region 111..112  
FT /note= "complementarity determining region 2"  
FT region 113..121  
FT /label= FR3  
FT region 122..128  
FT /note= "complementarity determining region 3"  
FT region 129..147  
FT /label= FR4  
FT /note= "framework region 4"  
FT region 148..157  
FT /note= "mouse constant kappa region"

CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in the figure. The primers used for cDNA synthesis are  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region. In conjunction with  
CC an appropriate V-region primer. In addition, the VR primer Q97318  
CC was used to amplify the heavy chain and 58 heavy chain. The sequences  
CC of the PCR products were determined and the deduced AA sequences in  
CC R7970-R7971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC used here.  
CC Sequence 107 AA:

Query Match 13.88; Score 20; DB 14; Length 107;  
Best Local Similarity 100.00; Pred. No. 3.10e-16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in the figure. The primers used for cDNA synthesis are  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region. In conjunction with  
CC an appropriate V-region primer. In addition, the VR primer Q97318  
CC was used to amplify the heavy chain and 58 heavy chain. The sequences  
CC of the PCR products were determined and the deduced AA sequences in  
CC R7970-R7971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC used here.  
CC Sequence 107 AA:

Query Match 13.88; Score 20; DB 14; Length 107;  
Best Local Similarity 100.00; Pred. No. 3.10e-16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 56 agyrtfgrzrgdyatit 75  
76 SCVPRSSSSSSSSSSSS 95

Query 48  
56 agyrtfgrzrgdyatit 75  
76 SCVPRSSSSSSSSSSSS 95

RESULT 48  
ID: 14576 standard: Protein: 107 AA.  
DE: 21-DEC-1995 (first entry)  
DE: Light chain variable region for monoclonal antibody 504.  
DE: Monoclonal antibody; heavy metal; mercury; variable region;  
DE: Key molecule.  
PE: Location/Qualifiers  
FT peptide 1..24  
FT /label= sig\_peptide  
FT region 25..47  
FT /label= FR1  
FT region 48..58  
FT /note= "framework region 1"  
FT region 59..71  
FT /note= "complementarity determining region 1"  
FT region 72..84  
FT /label= FR2  
FT region 85..97  
FT /note= "framework region 2"  
FT region 98..110  
FT /label= CDR3  
FT region 111..112  
FT /note= "complementarity determining region 2"  
FT region 113..121  
FT /label= FR3  
FT region 122..128  
FT /note= "complementarity determining region 3"  
FT region 129..147  
FT /label= FR4  
FT /note= "framework region 4"

CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in the figure. The primers used for cDNA synthesis are  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region. In conjunction with  
CC an appropriate V-region primer. In addition, the VR primer Q97318  
CC was used to amplify the heavy chain and 58 heavy chain. The sequences  
CC of the PCR products were determined and the deduced AA sequences in  
CC R7970-R7971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC used here.  
CC Sequence 107 AA:

Query Match 13.88; Score 20; DB 14; Length 107;  
Best Local Similarity 100.00; Pred. No. 3.10e-16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Chain 5; P14 59; 28pp; English  
CC Murine monoclonal anti-idiotypic antibodies, 1598, 196 and 546 are  
CC new. They induce an immune response against epidermal growth factor  
CC receptor (EGFR). The sequences of the heavy and light chain variable  
CC regions of these antibodies are given in the specification. The  
CC sequences of the heavy and light chain variable regions of the  
CC tumours that express EGFR on their surface, including melanomas,  
CC gliomas and carcinomas.  
CC Sequence 147 AA:

Query Match 14.58; Score 21; DB 23; Length 147;  
Best Local Similarity 100.00; Pred. No. 1.72e-15;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 gttctctatadpvtatp 145  
121 CITEIRDAAPVPSIPPS 141

Query 47  
126 gttctctatadpvtatp 145  
121 CITEIRDAAPVPSIPPS 141

RESULT 47  
ID: 14576 standard: Protein: 107 AA.  
DE: 21-DEC-1995 (first entry)  
DE: Light chain variable region for monoclonal antibody 1910.  
DE: Monoclonal antibody; heavy metal; mercury; variable region;  
DE: Key molecule.  
PE: Location/Qualifiers  
FT peptide 1..24  
FT /label= sig\_peptide  
FT region 25..47  
FT /label= FR1  
FT region 48..58  
FT /note= "framework region 1"  
FT region 59..71  
FT /note= "complementarity determining region 1"  
FT region 72..84  
FT /label= FR2  
FT region 85..97  
FT /note= "framework region 2"  
FT region 98..110  
FT /label= CDR3  
FT region 111..112  
FT /note= "complementarity determining region 2"  
FT region 113..121  
FT /label= FR3  
FT region 122..128  
FT /note= "complementarity determining region 3"  
FT region 129..147  
FT /label= FR4  
FT /note= "framework region 4"

CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in the figure. The primers used for cDNA synthesis are  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region. In conjunction with  
CC an appropriate V-region primer. In addition, the VR primer Q97318  
CC was used to amplify the heavy chain and 58 heavy chain. The sequences  
CC of the PCR products were determined and the deduced AA sequences in  
CC R7970-R7971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC used here.  
CC Sequence 107 AA:

Query Match 13.88; Score 20; DB 14; Length 107;  
Best Local Similarity 100.00; Pred. No. 3.10e-16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in the figure. The primers used for cDNA synthesis are  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region. In conjunction with  
CC an appropriate V-region primer. In addition, the VR primer Q97318  
CC was used to amplify the heavy chain and 58 heavy chain. The sequences  
CC of the PCR products were determined and the deduced AA sequences in  
CC R7970-R7971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC used here.  
CC Sequence 107 AA:

Query Match 13.88; Score 20; DB 14; Length 107;  
Best Local Similarity 100.00; Pred. No. 3.10e-16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 56 agyrtfgrzrgdyatit 75  
76 SCVPRSSSSSSSSSSSS 95

Query 49  
56 agyrtfgrzrgdyatit 75  
76 SCVPRSSSSSSSSSSSS 95

RESULT 49  
ID: 14576 standard: Protein: 107 AA.  
DE: 21-DEC-1995 (first entry)  
DE: Light chain variable region for monoclonal antibody 1910.  
DE: Monoclonal antibody; heavy metal; mercury; variable region;  
DE: Key molecule.  
PE: Location/Qualifiers  
FT peptide 1..24  
FT /label= sig\_peptide  
FT region 25..47  
FT /label= FR1  
FT region 48..58  
FT /note= "framework region 1"  
FT region 59..71  
FT /note= "complementarity determining region 1"  
FT region 72..84  
FT /label= FR2  
FT region 85..97  
FT /note= "framework region 2"  
FT region 98..110  
FT /label= CDR3  
FT region 111..112  
FT /note= "complementarity determining region 2"  
FT region 113..121  
FT /label= FR3  
FT region 122..128  
FT /note= "complementarity determining region 3"  
FT region 129..147  
FT /label= FR4  
FT /note= "framework region 4"

CC the C kappa domain. Some of the primers used for cDNA synthesis are  
CC shown in the figure. The primers used for cDNA synthesis are  
CC variable region of a particular antibody polypeptide was also used  
CC for PCR amplification of that variable region. In conjunction with  
CC an appropriate V-region primer. In addition, the VR primer Q97318  
CC was used to amplify the heavy chain and 58 heavy chain. The sequences  
CC of the PCR products were determined and the deduced AA sequences in  
CC R7970-R7971. The descriptions of the SEQ ID nos given on pp 44-45  
CC and in the claims are different from the descriptions in the  
CC used here.  
CC Sequence 107 AA:

Query Match 13.88; Score 20; DB 14; Length 107;  
Best Local Similarity 100.00; Pred. No. 3.10e-16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



# MPREX

(TM)

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March: protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Apr 15 18:02:37 1999: MasPar time 5.59 Seconds  
Tabular output not generated. 656,750 Million cell updates/sec

Title: >US-08-836-453-2  
Description: (11-145) from US08836455.pep  
Percent Score: 154  
Sequence: 1 KAPPA10LPTLLPPTC...IKRADAPEVIPPSSK 145  
Scoring table: GAP 60  
Matrix: uniprottable

Searched: 74019 seqs, 26840355 residues

Post-processing: Minimum Match ON

Database: Listing first 1000 summaries

Statistics: Mean 3.465; Variance 0.458; scale 7.567

Pred. No. is the number of results predicted by chance to have a  
percent score of 154 or greater. The results are sorted by percent  
score and are displayed by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	29	20	0	130	1 RV5G_MOUSE IG KAPPA CHAIN PRECURS	1.46e-57

104	18	12	4	117	1 RV5H_MOUSE IG KAPPA CHAIN PRECURS	1.16e-06
105	16	11	0	117	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	1.16e-06
106	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
107	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
108	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
109	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
110	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
111	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
112	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
113	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
114	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
115	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
116	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
117	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
118	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
119	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
120	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
121	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
122	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
123	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
124	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
125	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
126	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
127	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
128	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
129	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
130	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
131	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
132	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
133	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
134	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
135	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
136	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
137	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
138	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
139	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
140	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
141	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
142	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
143	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
144	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
145	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
146	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
147	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
148	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
149	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
150	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
151	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
152	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
153	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21
154	16	11	0	129	1 RV1L_HUMAN IG KAPPA CHAIN PRECURS	2.64e-21



















RE BLOCHER, J. 123, 645-958(1971).  
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR: A01855; KIRIDE.  
 DB HSP: P01607; 1PVC.  
 RM IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 2 2 3 3  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 89  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 11664 MW; 1084493 CRC32;  
 Query Match 9.7%: Score 14; DB 1; Length 108;  
 Best Local Similarity 85.7%: Pred. No. 3,546-16;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 BIRNBOSSER, S. 14  
 OY 21 DICTYOSPASTIS 34

RESULT 19  
 ID KY15, MOUSE STANDARD: PRT: 108 AA.  
 AC P01610; 1PVC.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-REGION (J606).  
 DR HSP: P01607; 1PVC.  
 RM IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 89  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 1084493 CRC32;  
 Query Match 9.7%: Score 14; DB 1; Length 108;  
 Best Local Similarity 85.7%: Pred. No. 3,546-16;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 BIRNBOSSER, S. 14  
 OY 21 DICTYOSPASTIS 34

FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 8455AF00 CRC32;  
 Query Match 9.7%: Score 14; DB 1; Length 108;  
 Best Local Similarity 100.0%: Pred. No. 3,546-16;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 DICTYOSPASTIS 34  
 OY 21 DICTYOSPASTIS 34

RESULT 21  
 ID KY15, MOUSE STANDARD: PRT: 113 AA.  
 AC P01610; 1PVC.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-REGION (J606).  
 DR HSP: P01607; 1PVC.  
 RM IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 89  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 1084493 CRC32;  
 Query Match 9.7%: Score 14; DB 1; Length 113;  
 Best Local Similarity 100.0%: Pred. No. 3,546-16;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRROGOTILEIN 113  
 OY 115 PYRROGOTILEIN 128

Query Match 9.7%: Score 14; DB 1; Length 113;  
 Best Local Similarity 100.0%: Pred. No. 3,546-16;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRROGOTILEIN 113  
 OY 115 PYRROGOTILEIN 128

FT DOMAIN 98 108  
 FT DISULFID 23 88  
 FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 11610 MW; 8398947 CRC32;  
 Query Match 9.7%: Score 14; DB 1; Length 108;  
 Best Local Similarity 100.0%: Pred. No. 3,546-16;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 95 PYRROGOTILEIN 108  
 OY 115 PYRROGOTILEIN 128

RESULT 20  
 ID KY15, MOUSE STANDARD: PRT: 108 AA.  
 AC P01610; 1PVC.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-REGION (J606).  
 DR HSP: P01607; 1PVC.  
 RM IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 89  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 1084493 CRC32;  
 Query Match 9.7%: Score 14; DB 1; Length 108;  
 Best Local Similarity 100.0%: Pred. No. 3,546-16;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRROGOTILEIN 113  
 OY 115 PYRROGOTILEIN 128

RESULT 22  
 ID KY15, MOUSE STANDARD: PRT: 113 AA.  
 AC P01610; 1PVC.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-REGION (J606).  
 DR HSP: P01607; 1PVC.  
 RM IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23  
 FT DOMAIN 2 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 89  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 1084493 CRC32;  
 Query Match 9.7%: Score 14; DB 1; Length 113;  
 Best Local Similarity 100.0%: Pred. No. 3,546-16;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRROGOTILEIN 113  
 OY 115 PYRROGOTILEIN 128

Query Match 9.7%: Score 14; DB 1; Length 113;  
 Best Local Similarity 100.0%: Pred. No. 3,546-16;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRROGOTILEIN 113  
 OY 115 PYRROGOTILEIN 128

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[illegible]

Q	Query Match	Seq. Local Similarity	92.3%	Score 13: DB 1: Length 108;
50	SEQUENCE	106 AA; 11732 MW; 35AB8ED ENC32;		
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OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA: RODENTIA.  
 RB SEQUENCE.  
 RA HERBERT H., HERBERT H., CHANG J.Y., BRAUN D.G.:  
 MEDLINE: 85128969.  
 DR PIR: A01911; 1986.  
 DR HSP: P01679; 1986.  
 RM IMMUNOGLOBULIN V REGION: HYBRIDOMA.  
 FT DOMAIN 1 1 23  
 FT DOMAIN 2 24 38  
 FT DOMAIN 3 25 52  
 FT DOMAIN 4 26 66  
 FT DOMAIN 5 27 80  
 FT DOMAIN 6 28 94  
 FT DOMAIN 7 29 108  
 FT DOMAIN 8 30 122  
 FT DISULFID 31 32  
 FT NON\_TER 33 34  
 FT SEQUENCE 111 AA: 12042 MW: 765289D CRC32:  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 111;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 99 PYRGOCTINLEIK 111  
 Oy 115 PYRGOCTINLEIK 127

RESULT 29  
 ID RY1LMOUSE STANDARD: PRT: 111 AA.  
 AC P01664;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (CIRC 101).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA: RODENTIA.  
 RB SEQUENCE.  
 RA HERBERT H., HERBERT H., CHANG J.Y., BRAUN D.G.:  
 MEDLINE: 79012520.  
 DR PIR: A01911; 1986.  
 DR HSP: P01679; 1986.  
 RM IMMUNOGLOBULIN V REGION: HYBRIDOMA.  
 FT DOMAIN 1 1 23  
 FT DOMAIN 2 24 38  
 FT DOMAIN 3 25 52  
 FT DOMAIN 4 26 66  
 FT DOMAIN 5 27 80  
 FT DOMAIN 6 28 94  
 FT DOMAIN 7 29 108  
 FT DOMAIN 8 30 122  
 FT DISULFID 31 32  
 FT NON\_TER 33 34  
 FT SEQUENCE 111 AA: 12042 MW: 765289D CRC32:  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 111;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 99 PYRGOCTINLEIK 111  
 Oy 115 PYRGOCTINLEIK 127

Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 112;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRGOCTINLEIK 112  
 Oy 115 PYRGOCTINLEIK 127

RESULT 31  
 ID RY1LMOUSE STANDARD: PRT: 112 AA.  
 AC P01655;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (CIRC 101).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA: RODENTIA.  
 RB SEQUENCE.  
 RA HERBERT H., HERBERT H., CHANG J.Y., BRAUN D.G.:  
 MEDLINE: 79012520.  
 DR PIR: A01911; 1986.  
 DR HSP: P01679; 1986.  
 RM IMMUNOGLOBULIN V REGION: HYBRIDOMA.  
 FT DOMAIN 1 1 23  
 FT DOMAIN 2 24 38  
 FT DOMAIN 3 25 52  
 FT DOMAIN 4 26 66  
 FT DOMAIN 5 27 80  
 FT DOMAIN 6 28 94  
 FT DOMAIN 7 29 108  
 FT DOMAIN 8 30 122  
 FT DISULFID 31 32  
 FT NON\_TER 33 34  
 FT SEQUENCE 112 AA: 12054 MW: 765289D CRC32:  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 112;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRGOCTINLEIK 112  
 Oy 115 PYRGOCTINLEIK 127

RESULT 32  
 ID RY1LMOUSE STANDARD: PRT: 112 AA.  
 AC P01655;  
 DT 21-JUL-1986 (REL. 01, CREATED)

FT DOMAIN 1 1 23  
 FT DOMAIN 2 24 38  
 FT DOMAIN 3 25 52  
 FT DOMAIN 4 26 66  
 FT DOMAIN 5 27 80  
 FT DOMAIN 6 28 94  
 FT DOMAIN 7 29 108  
 FT DOMAIN 8 30 122  
 FT DISULFID 31 32  
 FT NON\_TER 33 34  
 FT SEQUENCE 112 AA: 11964 MW: A2064C7 CRC32:  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 111;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 99 PYRGOCTINLEIK 111  
 Oy 115 PYRGOCTINLEIK 127

RESULT 30  
 ID RY1LMOUSE STANDARD: PRT: 112 AA.  
 AC P01655;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-II REGION (CIRC 101).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA: RODENTIA.  
 RB SEQUENCE.  
 RA HERBERT H., HERBERT H., CHANG J.Y., BRAUN D.G.:  
 MEDLINE: 80955101.  
 DR PIR: A01911; 1986.  
 DR HSP: P01679; 1986.  
 RM IMMUNOGLOBULIN V REGION: HYBRIDOMA.  
 FT DOMAIN 1 1 23  
 FT DOMAIN 2 24 38  
 FT DOMAIN 3 25 52  
 FT DOMAIN 4 26 66  
 FT DOMAIN 5 27 80  
 FT DOMAIN 6 28 94  
 FT DOMAIN 7 29 108  
 FT DOMAIN 8 30 122  
 FT DISULFID 31 32  
 FT NON\_TER 33 34  
 FT SEQUENCE 112 AA: 12221 MW: C16D8265 CRC32:  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 112;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRGOCTINLEIK 112  
 Oy 115 PYRGOCTINLEIK 127

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (N1).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA: RODENTIA.  
 RB SEQUENCE.  
 RA HERBERT H., HERBERT H., CHANG J.Y., BRAUN D.G.:  
 MEDLINE: 79012520.  
 DR PIR: A01911; 1986.  
 DR HSP: P01679; 1986.  
 RM IMMUNOGLOBULIN V REGION: HYBRIDOMA.  
 FT DOMAIN 1 1 23  
 FT DOMAIN 2 24 38  
 FT DOMAIN 3 25 52  
 FT DOMAIN 4 26 66  
 FT DOMAIN 5 27 80  
 FT DOMAIN 6 28 94  
 FT DOMAIN 7 29 108  
 FT DOMAIN 8 30 122  
 FT DISULFID 31 32  
 FT NON\_TER 33 34  
 FT SEQUENCE 112 AA: 12346 MW: A105767 CRC32:  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 112;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRGOCTINLEIK 112  
 Oy 115 PYRGOCTINLEIK 127

RESULT 33  
 ID RY1LMOUSE STANDARD: PRT: 116 AA.  
 AC P01655;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)  
 DE IG KAPPA CHAIN V-I REGION (N1).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA: RODENTIA.  
 RB SEQUENCE.  
 RA HERBERT H., HERBERT H., CHANG J.Y., BRAUN D.G.:  
 MEDLINE: 80955101.  
 DR PIR: A01911; 1986.  
 DR HSP: P01679; 1986.  
 RM IMMUNOGLOBULIN V REGION: HYBRIDOMA.  
 FT DOMAIN 1 1 23  
 FT DOMAIN 2 24 38  
 FT DOMAIN 3 25 52  
 FT DOMAIN 4 26 66  
 FT DOMAIN 5 27 80  
 FT DOMAIN 6 28 94  
 FT DOMAIN 7 29 108  
 FT DOMAIN 8 30 122  
 FT DISULFID 31 32  
 FT NON\_TER 33 34  
 FT SEQUENCE 116 AA: 12346 MW: A105767 CRC32:  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1,08e-13; Length 116;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 100 PYRGOCTINLEIK 116  
 Oy 115 PYRGOCTINLEIK 127









OC EUMARTONIA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;  
 RN [1]  
 RP SEQUENCE: 79073152  
 RX MEDLINE: 79073152  
 RA WETTERER, W.; GATTAGLIA, L.; LOH, E.; SCHILLING, J.; HOOD, L.E.;  
 RL NATURE 276:785-790(1978).  
 CC -1- THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.  
 DR PIR: A01930; KMS480.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRANKMOR 1.  
 FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 59 FRANKMOR 2.  
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 5 92 FRANKMOR 3.  
 FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 7 101 FRANKMOR 4.  
 FT DISULFID 102 111 BY SIMILARITY.  
 FT NON\_TER 111 111  
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 Query Match 7.64; Score 11: DB 1: Length 111;  
 Best Local Similarity 100.0%; Pred. No. 6,366-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 101 TPGCCTLEIK 111  
 QY 117 TPGCCTLEIK 127

RESULT 49  
 ID EVL MOOSE STANDARD: PRT: 111 AA.  
 AC POL672.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1989 (REL. 01, LAST SEQUENCE UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 7940).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUMARTONIA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;  
 RN [1]  
 RP SEQUENCE: 79073152  
 RX MEDLINE: 79073152  
 RA WETTERER, W.; GATTAGLIA, L.; LOH, E.; SCHILLING, J.; HOOD, L.E.;  
 RL NATURE 276:785-790(1978).  
 CC -1- THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.  
 DR PIR: A01930; KMS480.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRANKMOR 1.  
 FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 59 FRANKMOR 2.  
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 5 92 FRANKMOR 3.  
 FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 102 111 BY SIMILARITY.  
 FT NON\_TER 111 111  
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 Query Match 7.64; Score 11: DB 1: Length 111;  
 Best Local Similarity 100.0%; Pred. No. 6,366-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 101 TPGCCTLEIK 111  
 QY 117 TPGCCTLEIK 127

Search completed: Thu Apr 15 18:03:29 1999  
 Job time : 52 secs.

FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 59 FRANKMOR 2.  
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 5 92 FRANKMOR 3.  
 FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 102 111 BY SIMILARITY.  
 FT NON\_TER 111 111  
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 Query Match 7.64; Score 11: DB 1: Length 111;  
 Best Local Similarity 100.0%; Pred. No. 6,366-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 101 TPGCCTLEIK 111  
 QY 117 TPGCCTLEIK 127

RESULT 50  
 ID EVL MOOSE STANDARD: PRT: 111 AA.  
 AC POL672.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1989 (REL. 01, LAST SEQUENCE UPDATE)  
 DE IG KAPPA CHAIN V-III REGION (PC 7940).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUMARTONIA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;  
 RN [1]  
 RP SEQUENCE: 79073152  
 RX MEDLINE: 79073152  
 RA WETTERER, W.; GATTAGLIA, L.; LOH, E.; SCHILLING, J.; HOOD, L.E.;  
 RL NATURE 276:785-790(1978).  
 CC -1- THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.  
 DR PIR: A01930; KMS480.  
 KW IMMUNOGLOBULIN V REGION.  
 FT DOMAIN 1 23 FRANKMOR 1.  
 FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 3 59 FRANKMOR 2.  
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 5 92 FRANKMOR 3.  
 FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING 3.  
 FT DISULFID 102 111 BY SIMILARITY.  
 FT NON\_TER 111 111  
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:  
 Query Match 7.64; Score 11: DB 1: Length 111;  
 Best Local Similarity 100.0%; Pred. No. 6,366-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

!!SEQUENCE LIST 1.0  
(Peptide) WORDSEARCH of: /home/obryen/reed455/olig/us-08-836-455-2 check: 4259 from: 1

FROMIG of: /home/obryen/reed455/olig/US08836455.pep  
sequence 2, application us/08836455

general information:  
applicant: chatterjee, malaya  
applicant: toon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: swp: \* Sequences: 254,782 Total-length: 82,009,484 April 18, 1999 20:25

Database Release Information:

2 databases: SWISS-PROT, Release 36.0, Released on 18Jul1998, Formatted on 18Aug1998  
Combined 2 SPTREMBL, Release 8.0, Released on 21Nov1998, Formatted on 15Dec1998

Word-size: 5 Words: 77835 Diagonals: 14,908 Total-diagonals: 118,698,092  
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 9.51

Sequence Stnd Diag Score Width Documentation ..

SM:KV5G_MOUSE	+	2	116	1	P01639	mus musculus (mouse).	1g kappa
SM:KV5H_MOUSE	+	2	70	1	P01641	mus musculus (mouse).	1g kappa
SM:KV5O_MOUSE	+	-20	46	1	P01648	mus musculus (mouse).	1g kappa
SM:KV5M_MOUSE	+	-20	46	1	P01646	mus musculus (mouse).	1g kappa
SM:KV5N_MOUSE	+	-20	45	1	P01647	mus musculus (mouse).	1g kappa
SM:KV5L_MOUSE	+	-20	45	1	P01645	mus musculus (mouse).	1g kappa
SM:KV5K_MOUSE	+	-20	45	1	P01644	mus musculus (mouse).	1g kappa
SM:KV5U_MOUSE	+	-20	40	1	P04946	mus musculus (mouse).	1g kappa
SM:KV1Y_HUMAN	+	-20	39	1	P80362	homo sapiens (human).	1g kappa
SM:KV5T_MOUSE	+	-20	38	1	P01653	mus musculus (mouse).	1g kappa
SM:KV5S_MOUSE	+	-20	38	1	P01652	mus musculus (mouse).	1g kappa
SM:KV5Q_MOUSE	+	-20	38	1	P01650	mus musculus (mouse).	1g kappa
SM:KV5P_MOUSE	+	-20	38	1	P01649	mus musculus (mouse).	1g kappa
SM:KV5J_MOUSE	+	-20	38	1	P01643	mus musculus (mouse).	1g kappa
SM:KV1R_HUMAN	+	-20	36	1	P01610	homo sapiens (human).	1g kappa
SM:KV5E_MOUSE	+	-20	36	1	P01637	mus musculus (mouse).	1g kappa
SM:KV1S_HUMAN	+	-20	35	1	P01611	homo sapiens (human).	1g kappa
SM:KV1G_HUMAN	+	-20	35	1	P01599	homo sapiens (human).	1g kappa
SM:KV1X_HUMAN	+	-20	34	1	P04432	homo sapiens (human).	1g kappa
SM:KV1O_HUMAN	+	-20	34	1	P01607	homo sapiens (human).	1g kappa
SM:KV1W_HUMAN	+	2	33	1	P04431	homo sapiens (human).	1g kappa
SM:KV5F_MOUSE	+	0	33	1	P01638	mus musculus (mouse).	1g kappa
SM:KV1A_HUMAN	+	-20	32	1	P01593	homo sapiens (human).	1g kappa
SM:KV1P_HUMAN	+	-20	31	1	P01608	homo sapiens (human).	1g kappa
SM:KV1H_HUMAN	+	-20	31	1	P01600	homo sapiens (human).	1g kappa
SM:KV5R_MOUSE	+	-20	29	1	P01651	mus musculus (mouse).	1g kappa
SM:KV1N_HUMAN	+	-20	28	1	P01606	homo sapiens (human).	1g kappa
SM:KV1V_HUMAN	+	-20	27	1	P04430	homo sapiens (human).	1g kappa
SM:KV1J_HUMAN	+	2	27	1	P01602	homo sapiens (human).	1g kappa
SM:KV1I_HUMAN	+	2	27	1	P01601	homo sapiens (human).	1g kappa
SM:KV1C_HUMAN	+	-20	27	1	P01595	homo sapiens (human).	1g kappa
SM:KV1D_HUMAN	+	-20	26	1	P01596	homo sapiens (human).	1g kappa
SM:KV5D_MOUSE	+	-20	26	1	P01636	mus musculus (mouse).	1g kappa
SM:KV1L_HUMAN	+	-20	25	1	P01604	homo sapiens (human).	1g kappa
SM:KV5C_MOUSE	+	0	25	1	P01635	mus musculus (mouse).	1g kappa
SM:KV1T_HUMAN	+	-20	24	2	P01612	homo sapiens (human).	1g kappa
SM:KV1Q_HUMAN	+	-20	24	1	P01609	homo sapiens (human).	1g kappa
SM:KV1B_HUMAN	+	-20	24	1	P01594	homo sapiens (human).	1g kappa
SM:KV6A_MOUSE	+	-21	24	2	P01675	mus musculus (mouse).	1g kappa
SM:KV3K_HUMAN	+	-21	24	2	P06311	homo sapiens (human).	1g kappa
SM:KV6D_MOUSE	+	-21	24	2	P01678	mus musculus (mouse).	1g kappa
SM:KV3D_MOUSE	+	-16	23	1	P03977	mus musculus (mouse).	1g kappa
SM:KV5B_MOUSE	+	-9	23	1	P01634	mus musculus (mouse).	1g kappa
SP_R0:P80913	+	3	23	2	P80913	mus musculus (mouse).	1g kappa
SM:KV1X_HUMAN	+	-20	22	1	P01605	homo sapiens (human).	1g kappa
SM:KV3C_MOUSE	+	-16	21	1	P01656	mus musculus (mouse).	1g kappa
SM:KV3A_MOUSE	+	-16	21	1	P01654	mus musculus (mouse).	1g kappa
SM:KV1F_HUMAN	+	-20	21	1	P01598	homo sapiens (human).	1g kappa
SM:KV1E_HUMAN	+	-20	21	1	P01597	homo sapiens (human).	1g kappa
SP_H0M:Q15533	+	-17	21	1	Q15533	homo sapiens (human).	dna real

*2 databases: SWISS-PROT, Release 36.0, Released on 18Jul1998, Formatted on 18Aug1998*  
*Combined 2 SPTREMBL, Release 8.0, Released on 21Nov1998, Formatted on 15Dec1998*  
*# of seqs - 77835, 14,908 total-diagonals: 118,698,092*  
*Word-size: 5 Words: 77835 Diagonals: 14,908 Total-diagonals: 118,698,092*  
*Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 9.51*

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561	6	4.1	9.11	3	009031	CLASS III CHITIN SYNTH
562	6	4.1	9.11	3	009030	CLASS III CHITIN SYNTH
563	6	4.1	9.15	4	060308	KIN4OS2 PROTEIN
564	6	4.1	9.25	4	060307	KIN4OS2 PROTEIN
565	6	4.1	9.42	4	045532	PRP FOR BT C. ELEGANS
566	6	4.1	9.42	4	045532	PRP FOR BT C. ELEGANS
567	6	4.1	9.42	4	045532	PRP FOR BT C. ELEGANS
568	6	4.1	9.63	4	011650	NOVEL PROTEIN KINASE P
569	6	4.1	9.63	4	011650	NOVEL PROTEIN KINASE P
570	6	4.1	9.63	4	011650	NOVEL PROTEIN KINASE P
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617	6	4.1	9.63	4	011650	NOVEL PROTEIN KINASE P
618	6	4.1	9.63	4	011650	NOVEL PROTEIN KINASE P
619	6	4.1	9.63	4	011650	NOVEL PROTEIN KINASE P
620	6	4.1	9.63	4	011650	NOVEL PROTEIN KINASE P
621						

611	6	4.1	3.1	3.1	603216	PUTING BODY-SPECIFIC	1.6
610	6	4.1	3.1	3.1	603217	PHOSIN VILA	1.6
609	6	4.1	3.1	3.1	603218	PHOSIN VILA	1.6
608	6	4.1	3.1	3.1	603219	PHOSIN VILA	1.6
607	6	4.1	3.1	3.1	603220	PHOSIN VILA	1.6
606	6	4.1	3.1	3.1	603221	PHOSIN VILA	1.6
605	6	4.1	3.1	3.1	603222	PHOSIN VILA	1.6
604	6	4.1	3.1	3.1	603223	PHOSIN VILA	1.6
603	6	4.1	3.1	3.1	603224	PHOSIN VILA	1.6
602	6	4.1	3.1	3.1	603225	PHOSIN VILA	1.6
601	6	4.1	3.1	3.1	603226	PHOSIN VILA	1.6
600	6	4.1	3.1	3.1	603227	PHOSIN VILA	1.6
599	6	4.1	3.1	3.1	603228	PHOSIN VILA	1.6
598	6	4.1	3.1	3.1	603229	PHOSIN VILA	1.6
597	6	4.1	3.1	3.1	603230	PHOSIN VILA	1.6
596	6	4.1	3.1	3.1	603231	PHOSIN VILA	1.6
595	6	4.1	3.1	3.1	603232	PHOSIN VILA	1.6
594	6	4.1	3.1	3.1	603233	PHOSIN VILA	1.6
593	6	4.1	3.1	3.1	603234	PHOSIN VILA	1.6
592	6	4.1	3.1	3.1	603235	PHOSIN VILA	1.6
591	6	4.1	3.1	3.1	603236	PHOSIN VILA	1.6
590	6	4.1	3.1	3.1	603237	PHOSIN VILA	1.6
589	6	4.1	3.1	3.1	603238	PHOSIN VILA	1.6
588	6	4.1	3.1	3.1	603239	PHOSIN VILA	1.6
587	6	4.1	3.1	3.1	603240	PHOSIN VILA	1.6
586	6	4.1	3.1	3.1	603241	PHOSIN VILA	1.6
585	6	4.1	3.1	3.1	603242	PHOSIN VILA	1.6
584	6	4.1	3.1	3.1	603243	PHOSIN VILA	1.6
583	6	4.1	3.1	3.1	603244	PHOSIN VILA	1.6
582	6	4.1	3.1	3.1	603245	PHOSIN VILA	1.6
581	6	4.1	3.1	3.1	603246	PHOSIN VILA	1.6
580	6	4.1	3.1	3.1	603247	PHOSIN VILA	1.6
579	6	4.1	3.1	3.1	603248	PHOSIN VILA	1.6
578	6	4.1	3.1	3.1	603249	PHOSIN VILA	1.6
577	6	4.1	3.1	3.1	603250	PHOSIN VILA	1.6
576	6	4.1	3.1	3.1	603251	PHOSIN VILA	1.6
575	6	4.1	3.1	3.1	603252	PHOSIN VILA	1.6
574	6	4.1	3.1	3.1	603253	PHOSIN VILA	1.6
573	6	4.1	3.1	3.1	603254	PHOSIN VILA	1.6
572	6	4.1	3.1	3.1	603255	PHOSIN VILA	1.6
571	6	4.1	3.1	3.1	603256	PHOSIN VILA	1.6
570	6	4.1	3.1	3.1	603257	PHOSIN VILA	1.6
569	6	4.1	3.1	3.1	603258	PHOSIN VILA	1.6
568	6	4.1	3.1	3.1	603259	PHOSIN VILA	1.6
567	6	4.1	3.1	3.1	603260	PHOSIN VILA	1.6
566	6	4.1	3.1	3.1	603261	PHOSIN VILA	1.6
565	6	4.1	3.1	3.1	603262	PHOSIN VILA	1.6
564	6	4.1	3.1	3.1	603263	PHOSIN VILA	1.6
563	6	4.1	3.1	3.1	603264	PHOSIN VILA	1.6
562	6	4.1	3.1	3.1	603265	PHOSIN VILA	1.6
561	6	4.1	3.1	3.1	603266	PHOSIN VILA	1.6

662	3	118	5	01968	CONSD F11C10.	3.16e+03
663	3	103	5	02041	P4424	3.16e+03
664	3	103	5	02042	RIBOSOMAL PROTEIN S4 (	3.16e+03
665	3	104	2	02054	CONSD F10B	3.16e+03
666	3	180	8	02100	SUBUNIT I OF CYTOCHROME	3.16e+03
667	3	146	5	02080	CONSD F489.	3.16e+03
668	3	153	1	02085	RIBOSOMAL PROTEIN S4 (	3.16e+03
669	3	153	1	02086	CONSD F489	3.16e+03
670	3	201	6	02101	LEUKEMIA INHIBITOR PA	3.16e+03
671	3	204	11	064015	IRON NITROGENASE [F8AG	3.16e+03
672	3	211	2	P94515	IRON NITROGENASE [F8AG	3.16e+03
673	3	214	6	021013	CONSD F0411	3.16e+03
674	3	227	5	021183	CONSD F0411	3.16e+03
675	3	227	5	021183	CONSD F0411	3.16e+03
676	3	217	9	063193	ORITHINE DECARBOXYLASE	3.16e+03
677	3	217	9	063193	ATP SYNTHASE A CHAIN (	3.16e+03
678	3	218	2	020817	CONSD F20B	3.16e+03
679	3	218	2	020817	CONSD F20B	3.16e+03
680	3	212	11	057531	MYOCTE ENHANCER FACTO	3.16e+03
681	3	212	11	071722	HYPOCRETALIN 27.1 NP	3.16e+03
682	3	212	11	071722	HYPOCRETALIN 27.1 NP	3.16e+03
683	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
684	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
685	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
686	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
687	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
688	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
689	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
690	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
691	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
692	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
693	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
694	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
695	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
696	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
697	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
698	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
699	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
700	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
701	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
702	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
703	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
704	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
705	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
706	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
707	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
708	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
709	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
710	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
711	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
712	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
713	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
714	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
715	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
716	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
717	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
718	3	264	7	030764	MYOCTE ENHANCER FACTO	3.16e+03
719	3	264	7			

713	338	4	000376	L1 ELEMENT 1,3 P40
714	338	4	000377	L1 ELEMENT 1,3 P40 A
715	338	4	015665	ORF1 COOR P40 40 ND
716	338	4	048725	TRANSPOSASE 37 8 ND
717	340	10	048725	TRANSPOSASE 37 8 ND
718	348	8	038774	REBLOSIS BISPHOSPHATE
719	348	8	001333	CYCLOCHROME B (P4AGENT
720	348	8	001333	CYCLOCHROME B (P4AGENT
721	350	2	034656	PRIMATE TRANSPOSASE
722	350	2	034656	PRIMATE TRANSPOSASE
723	355	3	023003	MATRAX (P4AGENT)
724	355	3	023003	MATRAX (P4AGENT)
725	355	3	023003	MATRAX (P4AGENT)
726	355	3	023003	MATRAX (P4AGENT)
727	360	8	020013	MATRAX (P4AGENT)
728	361	8	020015	MATRAX (P4AGENT)
729	365	5	020721	YENIS PROTEIN Y/PEPTIDE
730	373	13	071722	YENIS PROTEIN Y/PEPTIDE
731	373	13	071722	YENIS PROTEIN Y/PEPTIDE
732	376	8	031095	ALPHA-TUBULIN (P4AGENT
733	376	8	031095	ALPHA-TUBULIN (P4AGENT
734	376	8	031095	ALPHA-TUBULIN (P4AGENT
735	376	8	031095	ALPHA-TUBULIN (P4AGENT
736	380	11	045980	SPIN SYSTEM MANNTOL-8P
737	380	11	045980	SPIN SYSTEM MANNTOL-8P
738	380	11	045980	SPIN SYSTEM MANNTOL-8P
739	380	11	045980	SPIN SYSTEM MANNTOL-8P
740	381	5	045981	SPIN SYSTEM MANNTOL-8P
741	381	5	045981	SPIN SYSTEM MANNTOL-8P
742	381	5	045981	SPIN SYSTEM MANNTOL-8P
743	381	5	045981	SPIN SYSTEM MANNTOL-8P
744	381	5	045981	SPIN SYSTEM MANNTOL-8P
745	381	5	045981	SPIN SYSTEM MANNTOL-8P
746	381	5	045981	SPIN SYSTEM MANNTOL-8P
747	381	5	045981	SPIN SYSTEM MANNTOL-8P
748	381	5	045981	SPIN SYSTEM MANNTOL-8P
749	381	5	045981	SPIN SYSTEM MANNTOL-8P
750	381	5	045981	SPIN SYSTEM MANNTOL-8P
751	381	5	045981	SPIN SYSTEM MANNTOL-8P
752	381	5	045981	SPIN SYSTEM MANNTOL-8P
753	381	5	045981	SPIN SYSTEM MANNTOL-8P
754	381	5	045981	SPIN SYSTEM MANNTOL-8P
755	381	5	045981	SPIN SYSTEM MANNTOL-8P
756	381	5	045981	SPIN SYSTEM MANNTOL-8P
757	381	5	045981	SPIN SYSTEM MANNTOL-8P
758	381	5	045981	SPIN SYSTEM MANNTOL-8P
759	381	5	045981	SPIN SYSTEM MANNTOL-8P
760	381	5	045981	SPIN SYSTEM MANNTOL-8P
761	381	5	045981	SPIN SYSTEM MANNTOL-8P
762	381	5	045981	SPIN SYSTEM MANNTOL-8P
763	381	5	045981	SPIN SYSTEM MANNTOL-8P
764	381	5	045981	SPIN SYSTEM MANNTOL-8P
765	381	5	045981	SPIN SYSTEM MANNTOL-8P
766	381	5	045981	SPIN SYSTEM MANNTOL-8P
767	381	5	045981	SPIN SYSTEM MANNTOL-8P
768	381	5	045981	SPIN SYSTEM MANNTOL-8P
769	381	5	045981	SPIN SYSTEM MANNTOL-8P
770	381	5	045981	SPIN SYSTEM MANNTOL-8P
771	381	5	045981	SPIN SYSTEM MANNTOL-8P
772	381	5	045981	SPIN SYSTEM MANNTOL-8P
773	381	5	045981	SPIN SYSTEM MANNTOL-8P
774	381	5	045981	SPIN SYSTEM MANNTOL-8P
775	381	5	045981	SPIN SYSTEM MANNTOL-8P
776	381	5	045981	SPIN SYSTEM MANNTOL-8P
777	381	5	045981	SPIN SYSTEM MANNTOL-8P
778	381	5	045981	SPIN SYSTEM MANNTOL-8P
779	381	5	045981	SPIN SYSTEM MANNTOL-8P
780	381	5	045981	SPIN SYSTEM MANNTOL-8P
781	381	5	045981	SPIN SYSTEM MANNTOL-8P
782	381	5	045981	SPIN SYSTEM MANNTOL-8P
783	381	5	045981	SPIN SYSTEM MANNTOL-8P
784	381	5	045981	SPIN SYSTEM MANNTOL-8P
785	381	5	045981	SPIN SYSTEM MANNTOL-8P
786	381	5	045981	SPIN SYSTEM MANNTOL-8P
787	381	5	045981	SPIN SYSTEM MANNTOL-8P
788	381	5	045981	SPIN SYSTEM MANNTOL-8P
789	381	5	045981	SPIN SYSTEM MANNTOL-8P
790	381	5	045981	SPIN SYSTEM MANNTOL-8P
791	381	5	045981	SPIN SYSTEM MANNTOL-8P





SEQUENCE FROM N.A.  
RC TISSUE-BONE-MARROW.  
RA DITZEL H.J., PAREN P.M.H.I., BINLEY J.M., SODROSKI T., MOORE J.P.,  
BA BARBAS C.F., BERTON D.R.:  
RL SUBMITTED (DEC-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U08047; G899073; 15.  
DR PFAM: PF00047; 19.  
FT NON\_TER 117 112  
SQ SEQUENCE 117 AA; 11905 MW; 40E0259D CRC32.

Query Match 8.3% Score 12; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.16e-09;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 TPOGCTLETER 109  
CY 117 TPOGCTLETER 128

RESULT 7  
ID C61251 PRELIMINARY: PRT: 127 AA.

AC 061251  
DT 01-NOV-1998 (TREMBL:01, CREATED)  
DT 01-NOV-1998 (TREMBL:01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBL:01, LAST ANNOTATION UPDATE)  
DE ANTIGEN, B-CELL RECEPTOR PROCDOR.  
OS MUS MUSCULUS (MURUS).  
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C;  
RX MEDLINE: 9613409  
RA KOTTERMAN R.E., WING M.G., WINTER G.:  
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: L43568; G899073; 15.  
DR PFAM: PF00047; 19.  
FT NON\_TER 120 127  
SQ SEQUENCE 127 AA; 13656 MW; C06E0809 CRC32.

Query Match 8.3% Score 12; DB 11; Length 127;  
Best Local Similarity 100.0%; Pred. No. 1.16e-09;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 115 TPOGCTLETER 126  
CY 117 TPOGCTLETER 128

Query Match 8.3% Score 12; DB 11; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.16e-09;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 118 TPOGCTLETER 149  
CY 25 TPOGCTLETER 36

RESULT 10  
ID C00288 PRELIMINARY: PRT: 244 AA.

AC 000288  
DT 01-JUL-1997 (TREMBL:04, CREATED)  
DT 01-JUL-1997 (TREMBL:04, LAST SEQUENCE UPDATE)  
DT 01-JUL-1997 (TREMBL:04, LAST ANNOTATION UPDATE)  
DE SINGLE-CHAIN TV FRAGMENT (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
RN (1)  
RP SEQUENCE FROM N.A.  
RC KOTTERMAN R.E., WING M.G., WINTER G.:  
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: L43568; G899073; 15.  
DR PFAM: PF00047; 19.  
FT NON\_TER 244 244  
SQ SEQUENCE 244 AA; 26127 MW; ACF2148B CRC32.

Query Match 8.3% Score 12; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 1.16e-09;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 233 TPOGCTLETER 244  
CY 117 TPOGCTLETER 128

RESULT 11  
ID C99514 PRELIMINARY: PRT: 105 AA.

AC 099514  
DT 01-NOV-1998 (TREMBL:03, CREATED)  
DT 01-NOV-1998 (TREMBL:03, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBL:03, LAST ANNOTATION UPDATE)  
DE LIGHT CHAIN FIB FRAGMENT (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
RN (1)  
RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.  
RC TISSUE-BONE-MARROW.  
RA DITZEL H.J., PAREN P.M.H.I., BINLEY J.M., SODROSKI T., MOORE J.P.,  
BA BARBAS C.F., BERTON D.R.:  
RL SUBMITTED (DEC-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U08047; G899073; 15.  
DR PFAM: PF00047; 19.  
FT NON\_TER 117 112  
SQ SEQUENCE 117 AA; 11905 MW; 40E0259D CRC32.

Query Match 8.3% Score 12; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.16e-09;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 TPOGCTLETER 109  
CY 117 TPOGCTLETER 128

RESULT 8  
ID C00289 PRELIMINARY: PRT: 240 AA.

AC 000289  
DT 01-JUL-1997 (TREMBL:04, CREATED)  
DT 01-JUL-1997 (TREMBL:04, LAST SEQUENCE UPDATE)  
DT 01-JUL-1997 (TREMBL:04, LAST ANNOTATION UPDATE)  
DE SINGLE-CHAIN TV FRAGMENT (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
RN (1)  
RP SEQUENCE FROM N.A.  
RC KOTTERMAN R.E., WING M.G., WINTER G.:  
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: L43568; G899073; 15.  
DR PFAM: PF00047; 19.  
FT NON\_TER 240 240  
SQ SEQUENCE 240 AA; 25569 MW; 6472AC99 CRC32.

Query Match 7.6% Score 11; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.49e-07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 229 TPOGCTLETER 240  
CY 117 TPOGCTLETER 128

Query Match 7.6% Score 11; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.49e-07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 TPOGCTLETER 34  
CY 24 TPOGCTLETER 34

RESULT 12  
ID C99933 PRELIMINARY: PRT: 107 AA.

AC 099933  
DT 01-NOV-1998 (TREMBL:03, CREATED)  
DT 01-NOV-1998 (TREMBL:03, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBL:03, LAST ANNOTATION UPDATE)  
DE VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN  
OS HOMO SAPIENS (HUMAN).  
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
RN (1)  
RP SEQUENCE FROM N.A.  
RC KOTTERMAN R.E., WING M.G., WINTER G.:  
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: L43568; G899073; 15.  
DR PFAM: PF00047; 19.  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11468 MW; 3D1FE815 CRC32.

Query Match 7.6% Score 11; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.49e-07;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4 TPOGCTLETER 14  
CY 24 TPOGCTLETER 34

RESULT 13  
ID C99980 PRELIMINARY: PRT: 107 AA.

AC 099980

DT 01-MAY-1997 (TREMBLIER, 03, CREATED)  
 DT 01-MAY-1997 (TREMBLIER, 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLIER, 06, LAST ANNOTATION UPDATE)  
 DE VASOACTIVE INTERSTITIAL POLYPEPTIDE HYDROLYZING AUTANTIBODY LIGHT CHAIN  
 DE HOMO SAPIENS (HUMAN)  
 DE HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUKARYOTA: PRIMATES  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE: 96375171.  
 RA TYUTYLKOVA S., GAO Q.S., THOMPSON A., BERNARD S., PAUL S.,  
 RL BLOCHIN, BIOPTIS, ACTA 1116:217-231(1996).  
 DR PRN: P00047, Q1650120, ..  
 FT NON\_TER 1 15  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA: 11925 MW: 61644A CRC32:  
 Query Match 7.6%: Score 11: DB 4: Length 107;  
 Best Local Similarity 100.0%: Pred. No. 1.49e-07;  
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 4 MTCSPSSLAS 14  
 QY 24 MTCSPSSLAS 34  
 RESULT 14  
 ID 041690 PRELIMINARY: PRT: 239 AA.  
 AC 041690 (TREMBLIER, 06, CREATED)  
 DT 01-JUN-1998 (TREMBLIER, 06, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLIER, 06, LAST ANNOTATION UPDATE)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUKARYOTA: PRIMATES  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE: 96375171.  
 RA TYUTYLKOVA S., GAO Q.S., THOMPSON A., BERNARD S., PAUL S.,  
 RL BLOCHIN, BIOPTIS, ACTA 1116:217-231(1996).  
 DR PRN: P00047, Q1650120, ..  
 FT NON\_TER 1 15  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA: 11925 MW: 61644A CRC32:  
 Query Match 7.6%: Score 11: DB 4: Length 107;  
 Best Local Similarity 100.0%: Pred. No. 1.49e-07;  
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 4 MTCSPSSLAS 14  
 QY 24 MTCSPSSLAS 34

DR PRN: P00047, 19.  
 FT NON\_TER 1 107  
 SQ SEQUENCE 107 AA: 11933 MW: 38775AC CRC32:  
 Query Match 6.9%: Score 10: DB 11: Length 107;  
 Best Local Similarity 100.0%: Pred. No. 1.61e-05;  
 Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 70 DIALYSIS 79  
 QY 90 DIALYSIS 99  
 RESULT 17  
 ID 097409 PRELIMINARY: PRT: 99 AA.  
 AC 097409 (TREMBLIER, 03, CREATED)  
 DT 01-JUN-1998 (TREMBLIER, 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLIER, 06, LAST ANNOTATION UPDATE)  
 DE TYPE II COLLAGEN ANTI-IDIOTYPIC ANTIBODY KAPPA LIGHT CHAIN VARIABLE  
 DE HOMO SAPIENS (HUMAN)  
 DE HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUKARYOTA: PRIMATES  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE: 97257994.  
 RA ITO H.O., UEDA T., HASHIMOTO T., INOKO T., KOGA T.,  
 RL EMIL, U6545, D131609, ..  
 DR PRN: P00047, 19.  
 FT NON\_TER 1 1  
 FT NON\_TER 99 99  
 SQ SEQUENCE 99 AA: 10956 MW: 880716F CRC32:  
 Query Match 6.2%: Score 9: DB 11: Length 99;  
 Best Local Similarity 100.0%: Pred. No. 1.42e-03;  
 Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 67 DIALYSIS 75  
 QY 90 DIALYSIS 98  
 RESULT 18  
 ID 014540 PRELIMINARY: PRT: 113 AA.  
 AC 014540 (TREMBLIER, 05, CREATED)  
 DT 01-JAN-1998 (TREMBLIER, 05, LAST SEQUENCE UPDATE)

Db 229 TPOGCTLEIR 239  
 QY 117 TPOGCTLEIR 127  
 RESULT 15  
 ID 041690 PRELIMINARY: PRT: 244 AA.  
 AC 041690 (TREMBLIER, 06, CREATED)  
 DT 01-JUN-1998 (TREMBLIER, 06, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBLIER, 06, LAST ANNOTATION UPDATE)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUKARYOTA: PRIMATES  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE: 96375171.  
 RA TYUTYLKOVA S., GAO Q.S., THOMPSON A., BERNARD S., PAUL S.,  
 RL BLOCHIN, BIOPTIS, ACTA 1116:217-231(1996).  
 DR PRN: P00047, Q1650120, ..  
 FT NON\_TER 1 15  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA: 11925 MW: 61644A CRC32:  
 Query Match 7.6%: Score 11: DB 4: Length 107;  
 Best Local Similarity 100.0%: Pred. No. 1.49e-07;  
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 234 TPOGCTLEIR 244  
 QY 117 TPOGCTLEIR 127  
 RESULT 16  
 ID 035538 PRELIMINARY: PRT: 107 AA.  
 AC 035538 (TREMBLIER, 05, CREATED)  
 DT 01-JAN-1998 (TREMBLIER, 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLIER, 06, LAST ANNOTATION UPDATE)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 DE ANTI-MP-SCFV (FRAGMENT)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUKARYOTA: PRIMATES  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE: 96375171.  
 RA TYUTYLKOVA S., GAO Q.S., THOMPSON A., BERNARD S., PAUL S.,  
 RL BLOCHIN, BIOPTIS, ACTA 1116:217-231(1996).  
 DR PRN: P00047, Q1650120, ..  
 FT NON\_TER 1 15  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA: 11925 MW: 61644A CRC32:  
 Query Match 7.6%: Score 11: DB 4: Length 107;  
 Best Local Similarity 100.0%: Pred. No. 1.49e-07;  
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 234 TPOGCTLEIR 244  
 QY 117 TPOGCTLEIR 127

DT 01-AUG-1998 (TREMBLIER, 07, LAST ANNOTATION UPDATE)  
 DE HOMO SAPIENS (HUMAN)  
 DE HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUKARYOTA: PRIMATES  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE: 97257994.  
 RA ITO H.O., UEDA T., HASHIMOTO T., INOKO T., KOGA T.,  
 RL EMIL, U6545, D131609, ..  
 DR PRN: P00047, 19.  
 FT NON\_TER 1 1  
 FT NON\_TER 99 99  
 SQ SEQUENCE 99 AA: 10956 MW: 880716F CRC32:  
 Query Match 6.2%: Score 9: DB 11: Length 99;  
 Best Local Similarity 100.0%: Pred. No. 1.42e-03;  
 Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 23 ONTOGSP 31  
 QY 23 ONTOGSP 31  
 RESULT 16  
 ID 015982 PRELIMINARY: PRT: 116 AA.  
 AC 015982 (TREMBLIER, 01, CREATED)  
 DT 01-NOV-1996 (TREMBLIER, 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBLIER, 06, LAST ANNOTATION UPDATE)  
 DE HEMATOPOIETIC FACTOR C LIGHT CHAIN (FRAGMENT)  
 DE HOMO SAPIENS (HUMAN)  
 DE HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUKARYOTA: PRIMATES  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE: 96375171.  
 RA TYUTYLKOVA S., GAO Q.S., THOMPSON A., BERNARD S., PAUL S.,  
 RL BLOCHIN, BIOPTIS, ACTA 1116:217-231(1996).  
 DR PRN: P00047, 19.  
 FT NON\_TER 1 1  
 FT NON\_TER 116 116  
 SQ SEQUENCE 116 AA: 11528 MW: 880716F CRC32:  
 Query Match 6.2%: Score 9: DB 4: Length 116;  
 Best Local Similarity 100.0%: Pred. No. 1.42e-03;  
 Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 1 DIONTOGSP 9

QY 21 DIONTOSPS 29

RESULT 20 PRELIMINARY: PRT: 113 AA.  
AC 014535: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 05, CREATED)  
DT 01-JAN-1998 (TREMBLAI, 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLAI, 07, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 113 113  
SQ SEQUENCE 113 AA: 12207 MW; A546C704 CRC32.

Query Match 5.5%: Score 8; DB 4; Length 113;  
Best Local Similarity 100.0%; Pred. No. 9.71e-02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 MTOGSPSL 31

RESULT 31 PRELIMINARY: PRT: 115 AA.  
AC 014537: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 05, CREATED)  
DT 01-JAN-1998 (TREMBLAI, 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLAI, 07, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 115 115  
SQ SEQUENCE 115 AA: 12417 MW; 96E3C279 CRC32.

RESULT 31 PRELIMINARY: PRT: 115 AA.  
AC 014537: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 05, CREATED)  
DT 01-JAN-1998 (TREMBLAI, 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLAI, 07, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 115 115  
SQ SEQUENCE 115 AA: 12417 MW; 96E3C279 CRC32.

Query Match 5.5%: Score 8; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 9.71e-02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GINLETER 129

RESULT 24 PRELIMINARY: PRT: 243 AA.  
AC 015140: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 05, CREATED)  
DT 01-JAN-1998 (TREMBLAI, 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLAI, 07, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 243 243  
SQ SEQUENCE 243 AA: 26235 MW; E0D5383 CRC32.

Query Match 5.5%: Score 8; DB 11; Length 243;  
Best Local Similarity 100.0%; Pred. No. 9.71e-02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GINLETER 128

Query Match 5.5%: Score 8; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 9.71e-02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 GINLETER 112

RESULT 22 PRELIMINARY: PRT: 118 AA.  
AC 014536: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 05, CREATED)  
DT 01-JAN-1998 (TREMBLAI, 05, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLAI, 07, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 118 118  
SQ SEQUENCE 118 AA: 12804 MW; CCE307A CRC32.

Query Match 5.5%: Score 8; DB 4; Length 118;  
Best Local Similarity 100.0%; Pred. No. 9.71e-02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GINLETER 115

RESULT 23 PRELIMINARY: PRT: 134 AA.  
AC 000619: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 04, CREATED)  
DT 01-JUN-1997 (TREMBLAI, 04, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLAI, 06, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 134 134  
SQ SEQUENCE 134 AA: 14534 MW; 9F08F98 CRC32.

RESULT 24 PRELIMINARY: PRT: 13 AA.  
AC 015536: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 01, CREATED)  
DT 01-JAN-1998 (TREMBLAI, 01, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLAI, 07, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 13 13  
SQ SEQUENCE 13 AA: 1406 MW; 71CE277 CRC32.

Query Match 4.8%: Score 7; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.85e-00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 GINLETER 99

RESULT 26 PRELIMINARY: PRT: 13 AA.  
AC 015536: 100.00% (100.00%)  
DT 01-JAN-1998 (TREMBLAI, 01, CREATED)  
DT 01-JAN-1998 (TREMBLAI, 01, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLAI, 07, LAST ANNOTATION UPDATE)  
DE HOMO SAPIENS (HUMAN)  
OS HOMO SAPIENS (HUMAN)  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: PRIMATES.  
RC TISSUE-PBL.  
RA TISSUE-PBL.  
RL SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF000471; F000471; D1023041.  
FT NON-TER 13 13  
SQ SEQUENCE 13 AA: 1406 MW; 71CE277 CRC32.

Query Match 4.8%: Score 7; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.85e-00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GINLETER 128

DB 2 TFGGCTK 8  
117 TFGGCTK 123

RESULT 27 PRELIMINARY: PRT: 109 AA.

ID 035337 (TREMBL:05, CREATED)  
DT 01-JUN-1998 (TREMBL:05, LAST SEQUENCE UPDATE)  
DE 01-JUN-1998 (TREMBL:05, LAST ANNOTATION UPDATE)  
OC EUTHERIA: RODENTIA.  
OS MYS MUSCULUS (MURINE).  
OC EUTHERIA: METAZOA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUTHERIA: RODENTIA.  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/C.

RA UDA T., HIFONI E., ISHIMARU M., MORIHARA F., ITOH T.;  
J. J. EMBRYO. STORE. 83:33-34(1997).

DR PPM: PPM0047.19.

FT NON-TER 109 109

SO SEQUENCE 109 AA: 11503 MW; EC7P076C CRC32:

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,854+00;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 100 PGGCTK 106  
OY 118 PGGCTK 124

RESULT 30 PRELIMINARY: PRT: 118 AA.

ID 035986 (TREMBL:01, CREATED)  
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)  
DE 01-NOV-1996 (TREMBL:01, LAST ANNOTATION UPDATE)  
OC EUTHERIA: PRIMATES.  
OS HOMO SAPIENS (HUMAN).  
OC EUTHERIA: METAZOA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUTHERIA: PRIMATES.  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/C.

RA ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;  
J. J. EMBRYO. STORE. 83:380-386(1993).

DR PPM: PPM0047.19.

FT NON-TER 118 118

SO SEQUENCE 118 AA: 12766 MW; D2815206 CRC32:

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,854+00;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 73 TFGGCTK 79  
OY 93 TFGGCTK 99

RESULT 31 PRELIMINARY: PRT: 121 AA.

ID 015984 (TREMBL:01, CREATED)  
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)  
DE 01-NOV-1996 (TREMBL:01, LAST ANNOTATION UPDATE)  
OC EUTHERIA: PRIMATES.  
OS HOMO SAPIENS (HUMAN).  
OC EUTHERIA: METAZOA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUTHERIA: PRIMATES.  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/C.

RA ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;  
J. J. EMBRYO. STORE. 83:380-386(1993).

DR PPM: PPM0047.19.

FT NON-TER 121 121

RL CANCER RES. 58:991-996(1998).

DR EMBL: X89990; E265408.

FT NON-TER 110 110

SO SEQUENCE 110 AA: 11392 MW; 761AD54A CRC32:

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,854+00;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 101 PGGCTK 107  
OY 118 PGGCTK 124

RESULT 32 PRELIMINARY: PRT: 114 AA.

ID 093336 (TREMBL:02, CREATED)  
DT 01-FEB-1997 (TREMBL:02, LAST SEQUENCE UPDATE)  
DE 01-FEB-1997 (TREMBL:02, LAST ANNOTATION UPDATE)  
OC EUTHERIA: RODENTIA.  
OS MYS MUSCULUS (MURINE).  
OC EUTHERIA: METAZOA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUTHERIA: RODENTIA.  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/C.

RA KASTEN T.L., WHITE S.A., NORTON T.T., BOND C.T., ADelman J.P.;  
J. J. EMBRYO. STORE. 83:113(1996).

DR PPM: PPM0047.19.

FT NON-TER 114 114

SO SEQUENCE 114 AA: 12123 MW; A3309D4 CRC32:

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,854+00;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 6 TFGGCTK 12  
OY 8 TFGGCTK 14

RESULT 33 PRELIMINARY: PRT: 158 AA.

ID 060411 (TREMBL:07, CREATED)  
DT 01-NOV-1996 (TREMBL:07, LAST SEQUENCE UPDATE)  
DE 01-NOV-1996 (TREMBL:07, LAST ANNOTATION UPDATE)  
OC EUTHERIA: PRIMATES.  
OS HOMO SAPIENS (HUMAN).  
OC EUTHERIA: METAZOA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUTHERIA: PRIMATES.  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/C.

RA LAMERLIN J.E., MCCRAY P.M., SHORRICK E., ADAMSON A.W.;  
J. J. EMBRYO. STORE. 83:113(1996).

DR PPM: PPM0047.19.

FT NON-TER 158 158

SO SEQUENCE 158 AA: 17635 MW; 01C6P4B CRC32:

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,854+00;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 9 TFGGCTK 15  
OY 7 TFGGCTK 13

RESULT 34 PRELIMINARY: PRT: 156 AA.

ID 048740 (TREMBL:06, CREATED)  
DT 01-JUN-1998 (TREMBL:06, LAST SEQUENCE UPDATE)  
DE 01-JUN-1998 (TREMBL:06, LAST ANNOTATION UPDATE)  
OC EUTHERIA: PRIMATES.  
OS HOMO SAPIENS (HUMAN).  
OC EUTHERIA: METAZOA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUTHERIA: PRIMATES.  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/C.







OY 139 PSSSLG 145  
 RESULT 45  
 ID Q46130 PRELIMINARY: PRT: 472 AA.  
 AC Q46130 (PRELIMINARY: 01, CREATED)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DE SERINE PROTEASE.  
 GN HTA.  
 OS CAMPYLOBACTER JELINT.  
 OC CAMPYLOBACTER JELINT.  
 OC AEROBIC, MOBILE, HELICAL, AND/OR VIBRIOID.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-81116, WOOD A.C., DERRY M.J., WERN R.V., KETTER J.J.  
 RU SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: X82658; E13368.  
 DE PFM: PFM0089; E13368.  
 DR PFM: PFM0089; E13368.  
 DE PROTEASE.  
 RN [1]  
 SQ SEQUENCE 472 AA: 50940 MW; 6636101 CRC32.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 4.85e+00; Length 472;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 101 SLSLSCV 107  
 OY 72 SLSLSCV 76  
 RESULT 46  
 ID Q35161 PRELIMINARY: PRT: 501 AA.  
 AC Q35161 (PRELIMINARY: 01, CREATED)  
 DT 01-JAN-1998 (PRELIMINARY: 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (PRELIMINARY: 05, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (PRELIMINARY: 07, LAST ANNOTATION UPDATE)  
 GN CERSL.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUMYOTIA: METACOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-81116, WOOD A.C., DERRY M.J., WERN R.V., KETTER J.J.  
 RU SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: X82658; E13368.  
 DE PFM: PFM0089; E13368.  
 DR PFM: PFM0089; E13368.  
 DE TISSUE-BRAIN:  
 RN [1]  
 SQ SEQUENCE 501 AA: 50940 MW; 6636101 CRC32.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 4.85e+00; Length 501;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 101 SLSLSCV 107  
 OY 72 SLSLSCV 76

OC EUMYOTIA: METACOA: ACCELONATES: NEBUTOD: SECRETINIA: RHADITIDA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-81116, WOOD A.C., DERRY M.J., WERN R.V., KETTER J.J.  
 RU SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: X82658; E13368.  
 DE PFM: PFM0089; E13368.  
 DR PFM: PFM0089; E13368.  
 DE TISSUE-BRAIN:  
 RN [1]  
 SQ SEQUENCE 501 AA: 50940 MW; 6636101 CRC32.  
 Query Match  
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 223 VELTCA 229  
 OY 39 VELTCA 45  
 RESULT 49  
 ID Q38755 PRELIMINARY: PRT: 665 AA.  
 AC Q38755 (PRELIMINARY: 01, CREATED)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (PRELIMINARY: 06, LAST ANNOTATION UPDATE)  
 DE ACETYLACETATE SYNTHASE PRECURSOR.  
 GN ACETYLACETATE SYNTHASE PRECURSOR.  
 OC EUMYOTIA: PLANTAE: EMBRYONOTA: MAGNOLIOPHYTA: MAGNOLIOPSIDA:  
 OC CARYOPHYLLALES: CARYOPHYLLALES: ANAETHALES.  
 RN [1]

RA HOOVER'S J.N.N., LITTLE P.P.R.:  
 RL GENOTYPE 45:97-104(1997).  
 DR EMBL: AF06014; G376400.  
 DE SEQUENCE 501 AA: 54331 MW; 8218028 CRC32.  
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 Best Local Similarity 100.0%; Pred. No. 4.85e+00; Length 501;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 449 TSSLSG 455  
 OY 71 TSSLSG 77  
 RESULT 47  
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 AC Q45913 (PRELIMINARY: 01, CREATED)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DE ORF 526.  
 GN RICKETTSIA BURNETI.  
 OS RICKETTSIA BURNETI.  
 OC RICKETTSIA BURNETI.  
 OC RICKETTSIA BURNETI.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-81116, WOOD A.C., DERRY M.J., WERN R.V., KETTER J.J.  
 RU SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: X84723; G682757.  
 DE ORF 526.  
 RN [1]  
 SQ SEQUENCE 526 AA: 58753 MW; 8684188 CRC32.  
 Query Match  
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 485 SLSLSCV 481  
 OY 29 SLSLSCV 35  
 RESULT 48  
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 AC P91243 (PRELIMINARY: 01, CREATED)  
 DT 01-MAY-1997 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-MAY-1997 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (PRELIMINARY: 07, LAST ANNOTATION UPDATE)  
 DE SIMILARITY TO A DNA-LINE DONOR.  
 GN P1311.7  
 OS CARNOMADITIS ELGANS.

RP SEQUENCE FROM N.A.  
 RC STRAIN-81116, WOOD A.C., DERRY M.J., WERN R.V., KETTER J.J.  
 RU SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: X84723; G682757.  
 DE ORF 526.  
 RN [1]  
 SQ SEQUENCE 591 AA: 58753 MW; 8684188 CRC32.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 4.85e+00; Length 591;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 64 TSPSSL 70  
 OY 25 TSPSSL 31  
 RESULT 50  
 ID Q27431 PRELIMINARY: PRT: 684 AA.  
 AC Q27431 (PRELIMINARY: 01, CREATED)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (PRELIMINARY: 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (PRELIMINARY: 06, LAST ANNOTATION UPDATE)  
 DE PROPHENOLINASE SUBUNIT 1 (EC 1.14.18.1) (MONOPEROXIDASE)  
 GN PROPHENOLINASE SUBUNIT 1 (EC 1.14.18.1) (MONOPEROXIDASE)  
 OC EUMYOTIA: METACOA: ANTHROPODA: INSECTA: LEPIDOPTERA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-81116, WOOD A.C., DERRY M.J., WERN R.V., KETTER J.J.  
 RU SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: X84723; G682757.  
 DE ORF 526.  
 RN [1]  
 SQ SEQUENCE 684 AA: 38028408 CRC32.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 4.85e+00; Length 684;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Apr 19 13:21:54 1999

us-08-036-455-2.rep1

Page 33

Db 201 DIGITAL 207  
OY 48 DIGITAL 54

Search completed: Thu Apr 15 18:04:57 1999  
Job time : 71 secs

!!SEQUENCE\_LIST 1.0  
(Nucleotide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-3 check: 9532 from:

FROMG of: /home/obryen/ree455/olig/us-08-836-455-3  
sequence 3, application us/08836455

general information:  
applicant: chatterjee, malaya  
applicant: foon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: geneseqn: \* Sequences: 240,622 Total-length: 94,065,609 April 18, 1999 22:14

Database Release Information:

Geneseq-NA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

Word-size: 15 Words: 70791 Diagonals: 2,313 Total diagonals: 409,502,538  
Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 30.25

Sequence Strd Diag Score Width Documentation ..

GENESON:T85150	+	0	461	1	Murine monoclonal anti-Idiotypic anti-
GENESON:N91146	+	38	288	1	2H7 Vh sequence. Polynucleotide(s) en
GENESON:T51042	+	71	288	1	Coding sequence for heavy chain variab
GENESON:V18593	+	71	288	1	Mouse 2H7 antibody heavy chain variab
GENESON:V03926	+	71	288	1	Mouse 2H7 antibody heavy chain variab
GENESON:V18557	+	71	288	1	Mouse 2H7 antibody heavy chain variab
GENESON:T36316	+	70	288	1	2H7 antibody heavy chain variable reg
GENESON:T70868	+	71	288	1	2H7 heavy chain variable sequence. Se
GENESON:N70971	+	39	245	2	2H7 VH sequence which contains JH1 se
GENESON:065631	+	0	215	1	Murine variable region heavy chain in
GENESON:065629	+	239	215	1	Vector contg. TCAE 8 DNA. Treating B
GENESON:062957	+	9	163	1	Anti-influenza N10 scfv. New target-h
GENESON:T35051	+	0	157	1	Mab VIL76 heavy chain (specific for
GENESON:N91645	+	63	149	1	Heavy chain of monoclonal antibody 6A
GENESON:066846	+	0	142	1	Sequence encoding the heavy chain var
GENESON:004695	+	38	139	1	Heavy chain variable domain of human
GENESON:Q12637	+	40	134	1	Monoclonal antibody OK3T heavy chain
GENESON:V54863	+	8	134	1	Murine antibody ICR-1.1 heavy chain
GENESON:V56413	+	8	134	1	Murine ICR-1.1 V-H region PCR product
GENESON:N91820	+	37	132	1	DNA sequence of the V and J regions
GENESON:Q32778	+	58	130	1	Heavy chain variable region of anti-F
GENESON:T39557	+	-60	127	1	Variable heavy chain cDNA for anti-hu
GENESON:T69541	+	-60	127	1	Anti-human FasL antibody (NOK5) heavy
GENESON:T77137	+	804	122	1	Single chain antigen hybrid receptor
GENESON:T05312	+	0	121	1	Mab SCH94.03 heavy chain DNA. Monoclo
GENESON:T77139	+	-45	119	1	Single chain antigen hybrid receptor
GENESON:T15802	+	-57	114	1	LL2 Mab VH region DNA. Chimeric and h
GENESON:T88129	+	-57	114	1	Variable heavy chain of Mab LL2 DNA.
GENESON:V00687	+	-54	114	1	Fusion gene sequence encoding anti-Ta
GENESON:T87815	+	-69	114	1	Antibody 7G12 heavy chain variable re
GENESON:V01097	+	0	113	1	Heavy chain variable region of mouse
GENESON:039234	+	-57	112	1	GMP-140 Mab heavy chain coding sequen
GENESON:V11399	+	-51	111	1	Human CD30 binding protein cDNA. Poly
GENESON:038877	+	0	110	1	CTMO1 VH cDNA. Anti-human milk fat gl
GENESON:T85854	+	131	109	1	Anti-HMG Mab CTMO1 heavy chain varia
GENESON:T58328	+	-57	109	1	Ber-H2 heavy gamma chain. DNA mols.
GENESON:T13270	+	312	109	1	Mucin-type synthetic glycolipid antih
GENESON:073678	+	44	108	1	Fv(GP-2) immunosuppressive. Immunosu
GENESON:T58327	+	0	108	1	Ber-H2 heavy gamma chain. DNA mols.
GENESON:T19086	+	55	106	1	Nucleotide sequence of the heavy cha
GENESON:079930	+	-12	105	1	Anti-tobacco mosaic virus monoclonal
GENESON:V09805	+	0	104	1	DNA encoding the heavy chain of the c
GENESON:015164	+	-39	103	1	VH186 region of anti-nitrophenylacety
GENESON:023863	+	-39	103	1	SCFVB18 construct mutant #5. Producti
GENESON:023862	+	-39	103	1	SCFVB18 construct mutant #5. Producti
GENESON:023861	+	-39	103	1	SCFVB18 construct mutant #4. Producti
GENESON:023860	+	-39	103	1	SCFVB18 construct mutant #4. Producti
GENESON:023859	+	-39	103	1	SCFVB18 construct mutant #2. Producti
GENESON:023858	+	-39	103	1	SCFVB18 construct mutant #2. Producti
GENESON:021100	+	-39	103	1	SCFVB18 construct. Producing members

*15 nt long*

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PS Example IV, Fig 21: 98pp: English.  
CC The present sequence was used in the development of a novel method  
CC for the production of an immunoglobulin (Ig) fragment capable of  
CC binding an antigen. The method comprises culturing an E. coli host  
CC cell expressing a recombinant DNA construct encoding a variable  
CC region of an Ig light chain, where (a) and (b) are operably linked  
CC to a single prokaryotic promoter to form a dicistronic  
CC construct. The construct is then transformed into a suitable host  
CC cell, such as E. coli, to produce a recombinant antibody 2H7 raised  
CC against human B-cell surface antigen. The invention provides a  
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CC properties. The method is applicable to the production of  
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CC specific Ig chains in various organisms. The application of  
CC the method to the production of large scale production of human  
CC monoclonal antibodies for the production of a solution to  
CC the problem of class switching antibody molecules.  
SQ Sequence 491 BP: 113 A: 152 C: 113 G: 113 T:  
Query Match 17.6% Score 81: DB 40: Length 491:  
Best Local Similarity 98.6%: Pred. No. 1,306-53:  
Matches 141: Conservative 0: Mismatches 2: Indels 0: Gaps 0:  
DB 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 38 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 169 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 228  
CC 98 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 157  
CC 229 tggcctgggttgaagagagagcact 251  
CC 158 tgcctcctccctgctgctgctgctgctgctgctgctgctgctgctgctgct 180  
RESULT 4  
ID V01926 standard: cDNA, 491 BP.  
AD 01-JUN-1998 (first entry)  
DT 01-JUN-1998 (first entry)  
DE Mouse 2H7 antibody heavy chain variable region cDNA.  
KW Mouse: murine: heavy chain: variable region:

KW Immunoglobulin fragment production: Ig fragment production:  
KW monoclonal antibody 2H7, human B-cell surface antigen: 2H7.  
OS Mue sp.  
FN Key Location/Qualifiers  
FT 516:Peptide 17-118  
FT 129-491 a  
FT mat\_peptide /tag b  
PI US569493.A  
PD 22-DEC-1997: 450731  
PR 29-MAR-1990: US-501092  
PR 01-NOV-1995: US-793980  
PR 27-OCT-1985: WO-002269  
PR 14-JUL-1987: US-012028  
PR 11-JUN-1987: US-012028  
PR 08-DEC-1992: US-887555  
PR 18-AUG-1994: US-299085  
PR 25-MAY-1995: US-450731  
PI (KOMA) KOMA CORP.  
PI Wall R. Walcott CL.  
PI Wall R. Walcott CL.  
PI WPI: 98-031749/03.  
DR P-PSDB: M41070.  
PT transformed with dicistronic expression cassette  
PS Example IV, Fig 21: 98pp: English.  
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CC monoclonal antibodies for the production of a solution to  
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SQ Sequence 491 BP: 113 A: 152 C: 113 G: 113 T:  
Query Match 17.6% Score 81: DB 40: Length 491:  
Best Local Similarity 98.6%: Pred. No. 1,306-53:  
Matches 141: Conservative 0: Mismatches 2: Indels 0: Gaps 0:  
DB 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 38 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 169 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 228  
CC 98 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 157  
CC 229 tggcctgggttgaagagagcact 251  
CC 158 tgcctcctccctgctgctgctgctgctgctgctgctgctgctgctgctgct 180  
RESULT 5  
ID V18593 standard: cDNA, 491 BP.  
AD 05-JUN-1998 (first entry)  
DT 05-JUN-1998 (first entry)  
DE Mouse 2H7 antibody heavy chain variable region cDNA.  
KW Mouse: murine: heavy chain: variable region: Ig fragment production:  
KW monoclonal antibody 2H7, human B-cell surface antigen: 2H7.  
OS Mue sp.  
FN Key Location/Qualifiers  
FT 516:Peptide 17-118  
FT mat\_peptide /tag a  
FT mat\_peptide /tag b  
PI US569493.A  
PD 22-DEC-1997: 450731  
PR 29-MAR-1990: US-501092  
PR 01-NOV-1995: US-793980  
PR 27-OCT-1985: WO-002269  
PR 14-JUL-1987: US-012028  
PR 11-JUN-1987: US-012028  
PR 08-DEC-1992: US-887555  
PR 18-AUG-1994: US-299085  
PR 25-MAY-1995: US-450731  
PI (KOMA) KOMA CORP.  
PI Wall R. Walcott CL.  
PI Wall R. Walcott CL.  
PI WPI: 98-031749/03.  
DR P-PSDB: M41070.  
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Query Match 17.6% Score 81: DB 40: Length 491:  
Best Local Similarity 98.6%: Pred. No. 1,306-53:  
Matches 141: Conservative 0: Mismatches 2: Indels 0: Gaps 0:  
DB 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 38 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 169 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 228  
CC 98 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 157  
CC 229 tggcctgggttgaagagagcact 251  
CC 158 tgcctcctccctgctgctgctgctgctgctgctgctgctgctgctgctgct 180  
RESULT 6  
ID T70868 standard: cDNA, 491 BP.  
AD 04-SEP-1997 (first entry)  
DT 04-SEP-1997 (first entry)  
DE 2H7 heavy chain variable sequence.  
KW Antibody engineering: heavy chain: light chain: chimeric antibody:

PS molecule and light chain.  
PS Example IV, Fig 21: 98pp: English.  
CC The present sequence was used in the development of a novel method  
CC for the production of an immunoglobulin (Ig) fragment capable of  
CC binding an antigen. The method comprises culturing an E. coli host  
CC cell expressing a recombinant DNA construct encoding a variable  
CC region of an Ig light chain, where (a) and (b) are operably linked  
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CC construct. The construct is then transformed into a suitable host  
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CC against human B-cell surface antigen. The invention provides a  
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CC desired variable region specificity and constant region  
CC properties. The method is applicable to the production of  
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CC monoclonal antibodies for the production of a solution to  
CC the problem of class switching antibody molecules.  
SQ Sequence 491 BP: 113 A: 152 C: 113 G: 113 T:  
Query Match 17.6% Score 81: DB 40: Length 491:  
Best Local Similarity 98.6%: Pred. No. 1,306-53:  
Matches 141: Conservative 0: Mismatches 2: Indels 0: Gaps 0:  
DB 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 109 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 38 taactacaggggtccatccaggtctatccagagctgggtgaggtggagc 168  
CC 169 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 228  
CC 98 ctgggtgaggtccaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 157  
CC 229 tggcctgggttgaagagagcact 251  
CC 158 tgcctcctccctgctgctgctgctgctgctgctgctgctgctgctgctgct 180



AD	RESULT	
AE	1.1113	standard: cDNA, 458 bp.
AF	1.1113	
AG	26-P23-1997	(first entry)
AH	Anti-idiotypic monoclonal antibody 1A7	variable heavy chain, cDNA.
AI	Murine; mouse; anti-idiotypic; monoclonal antibody (MAb); 1A7;	
AJ	extracellular chain; glycoprotein; cDNA; 116aa; neuroblastoma;	
AK	glioma; malignant melanoma; soft tissue sarcoma; small cell carcinoma;	
AL	vaccine; treatment; palliative; detection; diagnosis;	
AM	recombinant production; purification; probe; primer; assay;	
AN	amplification; gene therapy; as.	
AO	key molecule.	
AP	mat_papille	Location/Qualifiers
AQ	1..456	
AR	1.456	
AS	1.456	
AT	1.456	
AV	1.456	
AW	1.456	
AX	1.456	
AY	1.456	
AZ	1.456	
BA	1.456	
BB	1.456	
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BD	1.456	
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BK	1.456	
BL	1.456	
BM	1.456	
BN	1.456	
BO	1.456	
BP	1.456	
BQ	1.456	
BR	1.456	
BS	1.456	
BT	1.456	
BV	1.456	
BW	1.456	
BX	1.456	
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CB	1.456	
CC	1.456	
CD	1.456	
CE	1.456	
CF	1.456	
CG	1.456	
CH	1.456	
CI	1.456	
CJ	1.456	
CK	1.456	
CL	1.456	
CM	1.456	
CN	1.456	
CO	1.456	
CP	1.456	
CQ	1.456	
CR	1.456	
CS	1.456	
CT	1.456	
CU	1.456	
CV	1.456	
CW	1.456	
CX	1.456	
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CZ	1.456	
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DE	1.456	
DF	1.456	
DG	1.456	
DH	1.456	
DI	1.456	
DJ	1.456	
DK	1.456	
DL	1.456	
DM	1.456	
DN	1.456	
DO	1.456	
DP	1.456	
DQ	1.456	
DR	1.456	
DS	1.456	
DT	1.456	
DU	1.456	
DV	1.456	
DW	1.456	
DX	1.456	
DY	1.456	
DZ	1.456	
EA	1.456	
EB	1.456	
EC	1.456	
ED	1.456	
EE	1.456	
EF	1.456	
EG	1.456	
EH	1.456	
EI	1.456	
EJ	1.456	
EK	1.456	
EL	1.456	
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EO	1.456	
EP	1.456	
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ER	1.456	
ES	1.456	
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EX	1.456	
EY	1.456	
EZ	1.456	
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FF	1.456	
FG	1.456	
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FJ	1.456	
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FW	1.456	
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FZ	1.456	
GA	1.456	
GB	1.456	
GC	1.456	
GD	1.456	
GE	1.456	
GF	1.456	
GG	1.456	
GH	1.456	
GI	1.456	

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PR 27-OCT-1986 : D073259  
 PF 01-NOV-1985 : D0739360.  
 PA (ROB./J) ROBINSON R.R.  
 PI Robinson RB, Liu AY, Horvitz AR, Walli R.:  
 DR NPN; 87:35004/19.  
 PT Protein of p162.  
 PT DNA procedures, with chemico antibodies etc. related to cancer  
 specific antigens.  
 CS Example: Fig 21: 12bp. English.  
 CC The heavy chain constant antibody molecule comprising 2 light  
 CC chains and heavy chain regions. Coding sequences for the Ig chains  
 CC are also claimed. The invention provides consensus sequences of  
 CC light and heavy chain J regions useful in the design of cloning  
 CC immunoglobulin genes or heavy chain spacers or probes for identifying  
 CC the nature of design of a particular VHC. It may be capable of  
 CC hybridizing to all Ig mRNAs or genes containing a single specific J  
 CC sequence. UIC denotes universal immunoglobulin gene. 114 F:  
 SS Sequence: 459 BP. 115 G: 112 C:  
 Query Match 16.1% Score 74: DB 2: Length 459:  
 Best Local Similarity 98.5%; Prid No.3.4e+47;  
 Matches 149: Conservative 0: Mismatches 2: Indels 0: Gaps 0:  
 Db 84 agggcgccaccacagcgcgtctctcaaaaggcggggaatggcgccggtaggc 143  
 Oy 45 AGCGTCCACATCCCAGGCTTCATTCAACAAGTGCGAACCATAACTGGTAATGTGCAC 104  
 Db 144 ccaggcgagaatttcctcgcaaggaacttccccgcatacatlccgatlaaaaagcctg 203  
 Oy 105 cttcacgcacaaatgccatcccgaacacctgttgccctacaaatnccaatttaaacatcga 164  
 Db 204 gttacgaagacaagccctc 219  
 Oy 165 gcttaaaacgaacacact 180

**RESULT**  
 11  
 ID T9347 standard: CDNA; 861 BP.  
 DC 08-DEC-1987  
 DT 08-DEC-1987 (first entry)  
 RV Single chain anti-viral antibody encoding CDNA.  
 NV Gene therapy; antibody; immunization; human immunodeficiency virus;  
 NM HIV; human T-cell leukemia virus; ss.  
 OM MO867231-NL  
 PR 28-NOV-1986  
 PF 23-MAY-1986: D073931.

[illegible][illegible]

Mon Apr 19 13:23:56 1995

US-08-836-455-3.png

Page 36

PA	23-MAY-1995:	US-417610.
PB	(UTR)- UNIV ZEPHERSON THOMAS.	
PC	Dated by 01-08-2000 at NCBI.	
PD	Improved gene therapy using recombinant gene coding for an antibody	
PE	- for intracellular immunization against pathogens recognized by the	
PF	antibody - esp. human immunodeficiency virus HIV-1	
PG	The present sequence encompasses single chain anti-HIV antibody or a	
PH	constructed using variable domains of the heavy and light chains of a	
PI	murine monoclonal antibody against (HIV-1)HXB rev (the parent	
PJ	antibody). This is incorporated into a viral vector where the function	
PK	and so affects replication of the other virus (HIV). Rev is one of the	
PL	essential regulatory proteins of HIV; it binds to rev responsive elements	
PM	(RRE) and promotes the nuclear export, stabilisation and utilisation of	
PN	the viral RNA containing RRE. A novel gene therapy method has been of	
PO	an antibody (Ab) that is selectively specific for an intracellular (IC)	
PP	antigen associated with a disease. The method is used to prevent or abate	
PQ	can be used to inhibit the replication of a virus, such as human T-cell	
PR	leukemia virus or especially HIV-1, or of other pathogens, e.g.	
PS	bacteria, fungi. The method provides immunity before or after the	
PT	treatment of the disease and can be used to control the severity of	
PV	Sequence : 861 BP: 199 N: 234 C: 230 G: 198 T:	
QA	Query Match	
QB	Similarity 100.0% Score 67 DB 30: Length 861:	
QC	Matches 67 Conservative 0 Mismatches 0 Indels 0 Gaps 0	
QD	Db 792 ACTCTGGGTCACAGAAAGCCATCGATCGCTGTCTTCTCAGCAAGCACGCCGCCGCCTG 851	
QE	374 ATCTCATTTTGAATGAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 433	
QF	Db 852 CTCATCTC 858	
QG	434 TTTTCTTCT 440	
QH	RESULTS	
QI	12 standard CDNA, 861 BP.	
QJ	AC Q81500	
QK	DT 30-AUG-1995 (first entry)	
QL	SPY anti-rev sequence	
QM	NM Intracellular immunization of virus type 1, AIDS. Rev protein;	
QN	SV: antiviral activity. Gene construct: single chain antibody; PV:	
QO	Synthetic. resistance; cell immunity. Ref: 25.	























Query Match 9.3% Score 43 DB 18 Length 348  
Best Local Similarity 100.0% Pred. No. 7.69e-20  
Matches 43: Conservative 0 Mismatches 0 Gaps 0  
DB 41 cttgggacctcagtggaagatgctcagagctcctcctacac 83  
QY 98 cttgggacctcagtggaagatgctcagagctcctcctacac 140  
Search completed: Sat Apr 17 17:44:14 1999  
Job time : 271 secs.

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!!SEQUENCE LIST 1.0  
(Nucleotide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-3 check: 9532 from:

FROMIG of: /home/obryen/ree455/olig/us-08-836-455-3  
sequence 3, application us/08836455

general information:

applicant: chatterjee, malaya

applicant: toon, kenneth a.

applicant: chatterjee, sunil k. . .

TO: GenEMBL: \* Sequences: 602,539 Total-length: 1,199,477,030 April 18, 1999 21:41

Database Release Information:

GenBank, Release 110.0, Released on 14Dec1998, Formatted on 15Dec1998  
EMBL, Release 56.10, Released on 16Sep1998, Formatted on 15Dec1998

Word-size: 15 Words: 313215 Diagonals: 9,868 Total-diagonals: 2,000,000,000  
Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 118.14

Sequence Strd Diag Score Width Documentation ..

GB_PAT:109199	+	38	288	1	109199 Sequence 38 from Patent WO 890
GB_PAT:108811	+	38	288	1	108811 Sequence 12 from Patent WO 880
GB_PAT:105921	+	38	288	1	105921 Sequence 37 from Patent EP 027
GB_RO:MUSIGHXW	+	38	288	1	M17953 Mouse Ig rearranged H-chain V-
GB_RO:MMAIDHCH	+	-57	240	1	X64805 M.musculus mRNA for anti-id m
GB_RO:MUSY	+	-57	237	1	L48668 Mus musculus (cell line C3H/F2
GB_SY:XXU49832	+	375	233	1	U49832 Synthetic single chain Fv anti
GB_RO:MMMD01C	+	-57	230	1	273357 M.musculus mRNA for rearranged
GB_RO:MMMD52C	+	-57	230	1	273358 M.musculus mRNA for rearranged
GB_RO:MMIGGCVRI	+	-57	230	1	225457 M.musculus immunoglobulin gamm
GB_RO:MMIGGCVRE	+	-57	230	1	225449 M.musculus immunoglobulin gamm
GB_RO:MMIGGCVRD	+	-57	230	1	225447 M.musculus immunoglobulin gamm
GB_RO:MMIGGCVRG	+	-78	228	1	225453 M.musculus immunoglobulin gamm
GB_RO:MMIGGCVRF	+	-78	228	1	225451 M.musculus immunoglobulin gamm
GB_RO:MMIGGCVRC	+	-78	228	1	225445 M.musculus immunoglobulin gamm
GB_RO:MMIGGCVRB	+	-78	228	1	225443 M.musculus immunoglobulin gamm
GB_RO:MMAL	+	-57	217	1	L48680 Mus musculus (cell line C3H/F2
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GB_PAT:AR015963	+	0	215	1	AR015963 Sequence 5 from patent US 57
GB_PAT:AR015961	+	2400	215	1	AR015961 Sequence 2 from patent US 57
GB_PAT:AR000013	+	0	215	1	AR000013 Sequence 9 from patent US 57
GB_RO:AF025445	+	650	214	1	AF025445 Mus musculus clone BHS2.19
GB_RO:MMMD47C	+	-57	214	1	273342 M.musculus mRNA for rearranged
GB_RO:MMMD50C	+	-57	214	1	273339 M.musculus mRNA for rearranged
GB_RO:MMML7HC	+	-100	194	1	272457 M.musculus mRNA for immunoglob
GB_RO:MMLB4THEV	+	-40	183	1	X65773 M.musculus DNA for Ige antibod
GB_RO:AF045029	+	-57	180	1	AF045029 Mus musculus hybridoma 3C4
GB_RO:MUSIGHAEF	+	-57	172	1	M36225 Mouse Ig heavy-chain mRNA V re
GB_RO:MMU10410	+	9	163	1	U10410 Mus musculus recombinant anti
GB_PAT:A51507	+	0	157	1	A51507 Sequence 9 from Patent EP07198
GB_PAT:AF045500	+	0	151	1	AF045500 Mus musculus 4B8 monoclonal
GB_RO:MMIGVH5	+	43	150	1	X02458 Mouse germline immunoglobulin
GB_PAT:A13735	+	63	149	1	A13735 variable region of a monoclonal
GB_RO:MMIGVH6	+	43	149	1	X02459 Mouse germline immunoglobulin
GB_RO:MUSIGHALPA	+	48	149	1	M28834 Mus musculus Igc2a chain (anti
GB_RO:MMU22903	+	-21	148	1	U22903 Mus musculus anti-human inter
GB_RO:MUSIGHAAB	+	49	148	1	M19897 Mouse Ig rearranged gamma-chai
GB_RO:MUSIGHAAN	+	54	147	1	M19897 Mouse Ig rearranged gamma-chai
GB_PAT:AB007986	+	-51	147	1	AB007986 Mus musculus mRNA for single
GB_RO:MUSIGHVAA	+	-57	146	1	M97861 Mouse hybridoma Ig rearranged
GB_RO:MUSIGHBHI	+	37	145	1	D14628 Mouse mRNA for immunoglobulin
GB_RO:MMU01658	+	0	145	1	U01658 Mus musculus BALB/c anti-glyco
GB_RO:MUSANVVDJ	+	46	145	1	M37621 Mouse anti-DNA autoantibody va
GB_RO:MUSIGKCLP	+	48	145	1	M20835 Mouse IgM rearranged heavy-ch
GB_RO:MUSIGZM5	+	226	143	1	D14634 Mouse embryo DNA for immunogl
GB_PAT:545115	+	49	143	1	S45115 Ig VDJ H (active allele) [mice
GB_SY:XXU44796	+	-57	140	1	U44796 Synthetic construct single-ch
GB_PAT:A07953	+	38	139	1	A07953 Artificial sequence for anti-h
GB_PAT:MDIGVAP	+	-76	139	1	222064 M.domesticus IgG variable regi
GB_PAT:MDIGVAVO	+	-76	139	1	222062 M.domesticus IgG variable regi

not left containing matches at least 15 nt long

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Physiologist, Department of Medical and Physiological Chemistry,  
Hastings 3, Uppsala, 75123, Sweden

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
FEATURES

3 (bases 1 to 303)  
Mo J A, Bona C A, and Holmdahl R.  
Variable region gene selection of immunoglobulin C-expressing B  
cells with specificity for a defined epitope on type II collagen  
Eur J Immunol 23 (10), 2503-2510 (1993)

Location/Qualifiers  
1. 305 Mus musculus  
/strain="DBA/2"  
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1. 305  
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LPTQALTPNDSTSNFNRKATITINDSSFTNQLSLTSDAVTCANST"

BASE COUNT 80 a 79 c 19 g 09 t

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Matches 105: Conservative 0: Mismatches 1: Indels 0: Gaps 0:  
Db 41 CTGGGGCTAGTAAAGTCTCTGCAAGGCTTGGCAATTCACATTACATA 100  
QY 98 CTGGGGCTAGTAAAGTCTCTGCAAGGCTTGGCAATTCACATTACATA 157  
Db 101 TCCACTGGCTAAACGACACCTGACAGGCGCTGGAATGATATCA 147  
QY 158 TCCACTGGCTAAACGACACCTGACAGGCGCTGGAATGATATCA 204

RESULT 12 MHC/CYR 105 bp RNA ROD 13-OCT-1993  
DEFINITION Mammalian immunoglobulin gamma heavy chain (DBA/2) gene, V region.  
ACCESSION 23548  
ID 9407818  
KEYWORDS heavy chain; IgG gene; immunoglobulin; variable region.

Db 41 CTGGGGCTAGTAAAGTCTCTGCAAGGCTTGGCAATTCACATTACATA 100  
QY 98 CTGGGGCTAGTAAAGTCTCTGCAAGGCTTGGCAATTCACATTACATA 157  
Db 101 TCCACTGGCTAAACGACACCTGACAGGCGCTGGAATGATATCA 147  
QY 158 TCCACTGGCTAAACGACACCTGACAGGCGCTGGAATGATATCA 204

RESULT 13 MHC/CYR 353 bp RNA ROD 20-DEC-1986  
DEFINITION Mammalian mRNA for rearranged Ig heavy chain V region (J588  
ACCESSION 273339  
ID 913217  
KEYWORDS heavy chain; immunoglobulin superfamily; joining region; variable  
region.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryotes; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 353)  
AUTHORS Gilliland S, Pujawara H, Kikuchi N, Kohn R, Rose J, Muller M,  
Benoit C, Mathis D, Kishimoto T, Mak T W, and Rajewsky R.  
TITLE CD30 deficient mouse mutants  
JOURNAL Eur J Immunol 23 (8), 1966-1969 (1993)  
MEDLINE 9409207  
FEATURES Location/Qualifiers  
1. 353 Mus musculus  
/strain="J588"  
/note="partial V-D-J region"

REFERENCE 1 (bases 1 to 353)  
AUTHORS Gilliland S, Pujawara H, Kikuchi N, Kohn R, Rose J, Muller M,  
Benoit C, Mathis D, Kishimoto T, Mak T W, and Rajewsky R.  
TITLE CD30 deficient mouse mutants  
JOURNAL Eur J Immunol 23 (8), 1966-1969 (1993)  
MEDLINE 9409207  
FEATURES Location/Qualifiers  
1. 353 Mus musculus  
/strain="J588"  
/note="partial V-D-J region"

Physiologist, Department of Medical and Physiological Chemistry,  
Hastings 3, Uppsala, 75123, Sweden

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
FEATURES

3 (bases 1 to 303)  
Mo J A, Bona C A, and Holmdahl R.  
Variable region gene selection of immunoglobulin C-expressing B  
cells with specificity for a defined epitope on type II collagen  
Eur J Immunol 23 (10), 2503-2510 (1993)

Location/Qualifiers  
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Matches 105: Conservative 0: Mismatches 1: Indels 0: Gaps 0:  
Db 41 CTGGGGCTAGTAAAGTCTCTGCAAGGCTTGGCAATTCACATTACATA 100  
QY 98 CTGGGGCTAGTAAAGTCTCTGCAAGGCTTGGCAATTCACATTACATA 157  
Db 101 TCCACTGGCTAAACGACACCTGACAGGCGCTGGAATGATATCA 147  
QY 158 TCCACTGGCTAAACGACACCTGACAGGCGCTGGAATGATATCA 204

RESULT 14 MHC/CYR 315 bp RNA ROD 20-DEC-1986  
DEFINITION Mammalian mRNA for rearranged Ig heavy chain V region (J588  
ACCESSION 273340  
ID 913217  
KEYWORDS heavy chain; immunoglobulin superfamily; joining region; variable  
region.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryotes; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 353)  
AUTHORS Gilliland S, Pujawara H, Kikuchi N, Kohn R, Rose J, Muller M,  
Benoit C, Mathis D, Kishimoto T, Mak T W, and Rajewsky R.  
TITLE CD30 deficient mouse mutants  
JOURNAL Eur J Immunol 23 (8), 1966-1969 (1993)  
MEDLINE 9409207  
FEATURES Location/Qualifiers  
1. 353 Mus musculus  
/strain="J588"  
/note="partial V-D-J region"

REFERENCE 1 (bases 1 to 353)  
AUTHORS Gilliland S, Pujawara H, Kikuchi N, Kohn R, Rose J, Muller M,  
Benoit C, Mathis D, Kishimoto T, Mak T W, and Rajewsky R.  
TITLE CD30 deficient mouse mutants  
JOURNAL Eur J Immunol 23 (8), 1966-1969 (1993)  
MEDLINE 9409207  
FEATURES Location/Qualifiers  
1. 353 Mus musculus  
/strain="J588"  
/note="partial V-D-J region"





LOCUS 369 CTGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGACACCC 428  
 Db 360 A 360  
 OR 429 A 429

RESULT 21 357 bp mRNA ROD 07-JAN-1997  
 LOCUS Mus musculus (cell line C3H/FP-20) chromosome 12 anti-DNA antibody  
 DEFINITION Mus musculus mRNA.  
 ACCESSION L4658  
 SOURCE house mouse  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Kloc M.K., Alexander, A.L., Pappen, A.M., Plascaky, D.S. and  
 Gilkeson, G.S.  
 TITLE Differences in V kappa gene utilization and VH CDR3 sequence among  
 B cell clones from C3H/2F mice and lupus mice with nephritis  
 JOURNAL Eur J Immunol. 26 (9): 2225-2233 (1996)

FEATURES  
 MEDLINE 96409289  
 LOCATION/Qualifiers  
 source 1..357 name="Mus musculus"  
 /db\_xref="taxon:10090"  
 /cell\_line="C3H/FP-20"  
 /cell\_type="hybridoma"  
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BASE COUNT 94 A 88 G 85 C 1 otherz

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 QY 58 CAGCGCTTATACAGACCTGCGGCTGACCTGCTCTGCTGACCAAGAC 117  
 Db 61 TCGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGAC 120  
 QY 118 TCGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGAC 177  
 Db 121 CTT 123  
 |||

TITLE Direct Submission  
 JOURNAL Submitted (25-APR-1996) D.G. Schindler, Helmann Institute of  
 Science, Immunology, Recel St., 76100 Rehovot, ISRAEL  
 FEATURES  
 source 1..358  
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 /accession="U0244"  
 /db\_xref="taxon:10090"  
 /cell\_type="hybridoma"  
 CDS  
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 /protein\_end=358  
 /db\_xref="PDB:1J9963"  
 /translation="PELVPEGVVSCALGATVTVTIOMNDRPG  
 AMRWQCGVGRKATITADSSSTVHQLSLTSDSVAVPCVTVYRNYA  
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BASE COUNT 99 A 88 G 85 C 1 otherz  
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Query Match 12.8% Score 59: DB 29: Length 368:  
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 Db 308 TCGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGAC 365  
 QY 371 TCGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGAC 429

RESULT 24 381 bp mRNA ROD 23-JAN-1995  
 LOCUS anti-estradol antibody heavy chain variable region (clone G3)  
 DEFINITION [clone G3]  
 ACCESSION U0244  
 SOURCE house mouse  
 ORGANISM Mus sp. BALB/c spleen cell-SP20 hybridoma.

REFERENCE  
 AUTHORS Stilian, C.A., Lincon, P.J., Rouse, D.J., Decker, D.J., Kilman, N.R.  
 TITLE Specific human IgG1 and IgG2a clones produced from hybridoma cell  
 lines and murine spleen cells by PCR amplification  
 JOURNAL PCR Methods Appl. 3 (6): 330-331 (1994)  
 MEDLINE 9504022  
 REMARK Genbank staff at the National Library of Medicine created this

OR 178 CTT 180

RESULT 22 173511 360 bp DNA PAT 23-DEC-1997  
 LOCUS Sequence 14 from patent US 568579.  
 DEFINITION 173511  
 ACCESSION 9509562  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 AUTHORS Shant, S.Y., Rothermel, A. and Ramalingam, M.  
 TITLE Use of antibody/antigen interactions to protect biologically active  
 proteins and peptides  
 JOURNAL Patent: US 568579 A, 14 11-NOV-1997;  
 1..360/Qualifiers  
 source 1..360 name="unknown"  
 /organism="unknown"  
 ORIGIN 85 A 101 C 95 G 79 C

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 Best Local Similarity 100.0%  
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 QY 371 TCGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGAC 429

RESULT 23 368 bp mRNA ROD 20-FEB-1998  
 LOCUS Mus musculus mRNA for esterase immunoglobulin heavy chain variable  
 DEFINITION Mus musculus mRNA for esterase immunoglobulin heavy chain variable  
 ACCESSION X97533  
 SOURCE house mouse  
 ORGANISM Mus musculus

BASE COUNT 85 A 101 C 95 G 79 C

Query Match 12.8% Score 59: DB 22: Length 360:  
 Best Local Similarity 100.0%  
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 QY 371 TCGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGAC 429

entry [NCBI gi284713197] from the original journal article.  
 This sequence comes from Fig. 5A.  
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 /note="This sequence comes from Fig. 5A."  
 /codon\_start=1  
 /translation="EVQLQSGELVPGVSVSCALGATVTVTIOMNDRPG  
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BASE COUNT 100 A 93 C 100 G 86 C

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 Best Local Similarity 100.0%  
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 QY 371 TCGACATCTGCGGCTGACAGACCTGACCTGCTCTGCTGACCAAGAC 429

RESULT 25 384 bp mRNA ROD 23-MAR-1994  
 LOCUS House hybridoma is rearranged H-chain mRNA V-region, partial cds.  
 DEFINITION House hybridoma is rearranged H-chain mRNA V-region, partial cds.  
 ACCESSION M57861  
 SOURCE house mouse  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Lohman, K.L., Kieber-Emmons, T. and Kennedy, R.C.  
 TITLE Immunoglobulin heavy chain variable region (clone G3)  
 specific for hepatitis B virus surface antigen  
 JOURNAL J Biol Chem. 269 (1): 1-10 (1994)  
 MEDLINE 9504022  
 REMARK Genbank staff at the National Library of Medicine created this





REFERENCE 2 (bases 1 to 420)  
 AUTHORS Murine; A.M., Bulens, F., Bernier, H., Melien, L., Lijnen, R.R. and Collen, D.  
 TITLE Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer  
 JOURNAL Eur J Biochem 193 (3): 767-775 (1990)  
 MEDLINE 8106033  
 COMMENT This sequence is of cDNA corresponding to the antibody MA15 directed against human crosslinked human fibrin fragment-D dimer. Data kindly provided by Vandamme A.M.  
 FEATURES  
 Location/Qualifiers  
 1..420  
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 /clone\_11b="Lambda Zap1"  
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BASE COUNT 110 A 113 C 97 G 100 T  
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 QY 371 TGGACACTGGGCTGACGACACCTGACGACCTGCTCCGACCAACGACACCCCA 429

LOCUS 9193405  
 DEFINITION C-region: D-region: J-region: Immunoglobulin gamma-chain: heavy chain; processed gene.  
 SOURCE Mouse myeloma cell line X 63.Ag8 653j, cDNA to mRNA, clone H IV 92.  
 ORGANISM Mus musculus  
 Eukaryotes; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 REFERENCES  
 1. Murine; A.M., Bulens, F., Bernier, H., Melien, L., Lijnen, R.R. and Collen, D. (1990) Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer. Eur J Biochem 193 (3): 767-775 (1990)  
 JOURNAL  
 MEDLINE 8106033  
 COMMENT Draft entry for (1) kindly provided by P. Buckel, 31-JUL-1987.  
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 /db\_xref="taxon:10090"  
 25..31  
 /note="Ig gamma-1 chain signal peptide"  
 CDS  
 61g\_peptide  
 /note="Ig gamma-1 chain (VD4C) precursor"  
 /codon\_start=1  
 /db\_xref="taxon:10090"  
 /translation="MPPVLAAGVQVQSGSLVPSGSLTCTVSGPELVTCVHINRPGKGLMAYVWGSGSDYNAISIRLSINRDKSQVFFKNSIGNLQNDTAITYCANVGTSDYMDQCTSYVSAATPSTVTA"

BASE COUNT 121 A 119 C 126 G 114 T  
 ORIGIN  
 Query Match 12.8% Score 59: DB 29: Length 480:  
 Best Local Similarity 100.0% Pred. No. 2,376-377:  
 Matches 59: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 410 TGGACACTGGGCTGACGACACCTGACGACCTGCTCCGACCAACGACACCCCA 468  
 QY 371 TGGACACTGGGCTGACGACACCTGACGACCTGCTCCGACCAACGACACCCCA 429

RESULT 30  
 LOCUS 444 bp mRNA ROD 30-JUN-1987  
 DEFINITION Mouse Ig gamma-chain active V-region VD4C1 mRNA from hybridoma LA 13.2, V-H-81X family.  
 JOURNAL J Biol Chem 263:13502-13506 (1988)  
 MEDLINE 8199244  
 COMMENT C-region: D-region: J-region: V-region: Immunoglobulin gamma-chain: heavy chain; processed gene.  
 SOURCE Mouse myeloma cell line X 63.Ag8 653j, cDNA to mRNA, clone H IV 92.  
 ORGANISM Mus musculus  
 Eukaryotes; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 REFERENCES  
 1. Murine; A.M., Bulens, F., Bernier, H., Melien, L., Lijnen, R.R. and Collen, D. (1990) Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer. Eur J Biochem 193 (3): 767-775 (1990)  
 JOURNAL  
 MEDLINE 8106033  
 COMMENT This sequence is of cDNA corresponding to the antibody MA15 directed against human crosslinked human fibrin fragment-D dimer. Data kindly provided by Vandamme A.M.  
 FEATURES  
 Location/Qualifiers  
 1..444  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 1..37  
 /note="Ig gamma-chain signal peptide"  
 CDS  
 61g\_peptide  
 /note="Ig gamma-chain VD4C1 precursor"  
 /codon\_start=1  
 /db\_xref="taxon:10090"  
 /translation="MPPVLAAGVQVQSGSLVPSGSLTCTVSGPELVTCVHINRPGKGLMAYVWGSGSDYNAISIRLSINRDKSQVFFKNSIGNLQNDTAITYCANVGTSDYMDQCTSYVSAATPSTVTA"

BASE COUNT 114 A 115 C 108 G 107 T  
 ORIGIN  
 Query Match 12.8% Score 59: DB 29: Length 444:  
 Best Local Similarity 100.0% Pred. No. 2,376-377:  
 Matches 59: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 377 TGGACACTGGGCTGACGACACCTGACGACCTGCTCCGACCAACGACACCCCA 435  
 QY 371 TGGACACTGGGCTGACGACACCTGACGACCTGCTCCGACCAACGACACCCCA 429

LOCUS 480 bp mRNA ROD 01-SEP-1988  
 DEFINITION Mouse Ig gamma-1 chain mRNA V-region (VD4C) from hybridoma MAK33.  
 SOURCE Mouse myeloma cell line X 63.Ag8 653j, cDNA to mRNA, clone H IV 92.  
 ORGANISM Mus musculus  
 Eukaryotes; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 REFERENCES  
 1. Murine; A.M., Bulens, F., Bernier, H., Melien, L., Lijnen, R.R. and Collen, D. (1990) Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer. Eur J Biochem 193 (3): 767-775 (1990)  
 JOURNAL  
 MEDLINE 8106033  
 COMMENT Draft entry for (1) kindly provided by P. Buckel, 31-JUL-1987.  
 FEATURES  
 Location/Qualifiers  
 1..501  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 1..37  
 /note="Ig H-chain from c8 Ca 1.7 signal peptide"  
 CDS  
 61g\_peptide  
 /note="Ig H-chain from c8 Ca 1.7"  
 /codon\_start=1  
 /db\_xref="taxon:10090"  
 /translation="MPPVLAAGVQVQSGSLVPSGSLTCTVSGPELVTCVHINRPGKGLMAYVWGSGSDYNAISIRLSINRDKSQVFFKNSIGNLQNDTAITYCANVGTSDYMDQCTSYVSAATPSTVTA"

BASE COUNT 125 A 138 C 131 G 107 T  
 ORIGIN  
 Query Match 12.8% Score 59: DB 29: Length 501:  
 Best Local Similarity 100.0% Pred. No. 2,376-377:  
 Matches 59: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 312 TGGACACTGGGCTGACGACACCTGACGACCTGCTCCGACCAACGACACCCCA 390











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REFERENCE 1 (bases 1 to 433)  
 AUTHORS Hiltner, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Roman, M., Rittin, L., Rohlfing, T., Le, M., Lennon, G., Morris, M., Trevaughn, J., Watson, R., Williamson, A., Woldmann, P., and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson R.  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 High quality sequence atops: 291  
 This clone is available royalty-free through LBL; contact the IMAG Consortium (info@img.llnl.gov) for further information.  
 Location/Qualifiers  
 1..433 repeat="Homo sapiens"  
 /clone="278893"  
 /organism="Homo sapiens"

## FEATURES

source mRNA  
 BASE COUNT 149 a 80 c 65 g 139 t  
 ORIGIN  
 Query Match 4.3% Score 20; DB 19; Length 433;  
 Best Local Similarity 100.0%; Pred. No. 3.62e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 357 TACATCATGAGTTAGG 376  
 ||||||||||||||||||||  
 QY 235 TACATCATGAGTTAGG 254

RESULT 8  
 LOCUS A116128 552 bp mRNA EST 14-MAY-1997  
 DEFINITION A116128.1 Sources pregnant uterus NBRU Homo sapiens CDNA clone  
 PRECUDOR (HMAN), mRNA sequence.  
 ACCESSION A116128  
 GI 91671177  
 KEYWORDS EST  
 SOURCE human  
 ORGANISM Homo sapiens  
 Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae;

CP 188 CCGTCACGCTCTCTCT 169  
 ||||||||||||||||||||

RESULT 9  
 LOCUS H47534 478 bp mRNA EST 16-AUG-1995  
 DEFINITION YP78409.1 Homo sapiens CDNA clone 193525.5 similar to  
 SP-EST, CAMEL P39691 ELONGATION FACTOR 2.  
 ACCESSION 9233586  
 KEYWORDS EST  
 SOURCE human  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 478)  
 AUTHORS Hiltner, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Roman, M., Rittin, L., Rohlfing, T., Le, M., Lennon, G., Morris, M., Trevaughn, J., Watson, R., Williamson, A., Woldmann, P., and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson R.  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 High quality sequence atops: 333  
 This clone is available royalty-free through LBL; contact the IMAG Consortium (info@img.llnl.gov) for further information.  
 Location/Qualifiers  
 1..478 repeat="Homo sapiens"

## FEATURES

source mRNA  
 BASE COUNT 95 a 134 c 123 g 120 t 6 others

REFERENCE 1 (bases 1 to 552)  
 AUTHORS Hiltner, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Roman, M., Rittin, L., Rohlfing, T., Le, M., Lennon, G., Morris, M., Trevaughn, J., Watson, R., Williamson, A., Woldmann, P., and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson R.  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 High quality sequence atops: 333  
 This clone is available royalty-free through LBL; contact the IMAG Consortium (info@img.llnl.gov) for further information.  
 Location/Qualifiers  
 1..552 repeat="Homo sapiens"

## FEATURES

source mRNA  
 BASE COUNT 123 a 167 c 142 g 117 t 3 others  
 ORIGIN  
 Query Match 4.3% Score 20; DB 6; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 3.62e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 354 CCGTCACGCTCTCTCT 373  
 ||||||||||||||||||||  
 QY 100 CCGTCACGCTCTCTCT 118

RESULT 10  
 LOCUS A488443 208 bp mRNA EST 27-MAY-1998  
 DEFINITION A488443.1 Sources testis NBRU Homo sapiens CDNA clone 139474  
 similar to TR:008810 008810 05-118ED. mRNA sequence.  
 ACCESSION 92893983  
 KEYWORDS EST  
 SOURCE human  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 208)  
 AUTHORS NCI-CCAB http://www.ncbi.nlm.nih.gov/ncicgdb.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 NCI-CCAB  
 9600 Rockledge Drive  
 Bethesda, MD 20895  
 Email: robert.strausberg@nih.gov  
 CDNA Library Preparation: M. Sento Soares, Ph.D., M. Patricia Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 CDNA sequencing by: Washington University Genome Sequencing Center  
 Clone identification by: Washington University Genome Sequencing Center  
 found through the I.M.A.C.E. Consortium (info@img.llnl.gov) etc.  
 www-bio.llnl.gov/DBP/Imag/Imag.html  
 Trace considered overall poor quality.  
 Possible reversed clone. Subcloned into wrong strand  
 Seq primer: -40m3 fwd. RT from Acetabulum  
 High quality sequence stop. 1.  
 Location/Qualifiers  
 1..208 repeat="Homo sapiens"

## FEATURES

source mRNA  
 BASE COUNT 95 a 134 c 123 g 120 t 6 others

note="Vector: pT7D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA prepared from mRNA obtained from Clontech primer 15' fwd, Not I, and primed with a Not I oligo (dT)





RNA  
BASE COUNT 52 a 83 c 72 g 46 t 3 others  
ORIGIN  
Query Match 3.9% Score 18: DB 24: Length 256:  
Best Local Similarity 100.0%: Pred. No. 1.05e-04:  
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 115 GGCACCGCTCCGACG 132  
|||||  
397 GTCACCGCTCCGACG 414

RESULT 14  
LOCUS A136137 267 bp mRNA EST 21-APR-1997  
DEFINITION Homo sapiens lymph node I Homo sapiens cDNA 5' end similar to  
accession  
Accession A136137  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; Eukaryotes; Eukaryotes; Metazoa; Chordata;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
Hominidae;  
1 (bases 1 to 267)  
REFERENCE  
AUTHORS Adams M.D., Kellavag, A.R., Fietzmann, R.D., Pulner, R.A.,  
Bull, C.J., Lee, N.H., Kellavag, E.F., Weinstock, K.G., Cocayne, J.D.,  
Clayton, R., Sutton, G., Blake, A., Brandon, R.C., Man-Wai, C.,  
Fitzgerald, L.M., Fitzhugh, M.M., Fitchman, J., Hagedorn, L.D.,  
Glock, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,  
Kellavag, J.M., Kelley, J.C., Liu, L.-I., Karmali, S.M., Kestrick, J.M.,  
Phillips, C.A., Rader, E., Rader, T.R., Rader, T.R., Rader, T.R.,  
Small, K.V., Spisberg, T.A., Uetzel, T.R., Weinstock, K.G.,  
Bednarek, D.P., Celis, E., Fietzmann, R.D., Coleman, A.A., Collins, E.J.,  
He, M., Hu, J.S., Gnehm, J.M., Gnehm, J.M., Gnehm, J.M.,  
Kosak, D.L., Kuo, C.C., Kuo, C.C., Kuo, C.C., Kuo, C.C.,  
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, C.L., Rubin, S.M.,  
Pillon, P.J., Pannon, M.R., Rosen, C.A., Haseltine, M.A., Fields, C.,  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotide cDNA sequence  
9602680

TITLE  
JOURNAL MEDLINE  
COMMENT  
Other ESTs: TNC168356  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018509300  
Fax: 3018509305  
Email: arxiv@igrr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Seq Primer: M3 Reverse  
Location/Qualifiers  
1. 308  
/organism="Homo sapiens"  
/db\_xref="GeneID:137128"  
/db\_xref="AF001137:137128"  
/clone="11b-Ep1d1yuna"  
/dev="stage=adult"  
/dev="stage=adult"  
BASE COUNT 65 a 86 c 74 g 77 t 6 others  
ORIGIN  
Query Match 3.9% Score 18: DB 25: Length 108:  
Best Local Similarity 100.0%: Pred. No. 1.05e-04:  
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 185 GGCCTCCGACGACG 202  
|||||  
101 GGCCTCCGACGACG 118

COMMENT Other ESTs: TNC168350  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018509300  
Fax: 3018509305  
Email: arxiv@igrr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Seq primer: M3 Reverse  
Location/Qualifiers  
1. 308  
/organism="Homo sapiens"  
/db\_xref="GeneID:137128"  
/db\_xref="AF001137:137128"  
/clone="11b-Ep1d1yuna"  
/dev="stage=adult"  
/dev="stage=adult"  
BASE COUNT 46 a 84 c 74 g 55 t 8 others  
ORIGIN  
Query Match 3.9% Score 18: DB 25: Length 267:  
Best Local Similarity 100.0%: Pred. No. 1.05e-04:  
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 174 GTCACCGCTCCGACG 91  
|||||  
397 GTCACCGCTCCGACG 414

RESULT 15  
LOCUS A136144 308 bp mRNA EST 21-APR-1997  
DEFINITION Homo sapiens lymph node I Homo sapiens cDNA 5' end similar to  
accession  
Accession A136144  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; Eukaryotes; Eukaryotes; Metazoa; Chordata;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
Hominidae;  
1 (bases 1 to 308)  
REFERENCE  
AUTHORS Adams M.D., Kellavag, A.R., Fietzmann, R.D., Pulner, R.A.,  
Bull, C.J., Lee, N.H., Kellavag, E.F., Weinstock, K.G., Cocayne, J.D.,  
Clayton, R., Sutton, G., Blake, A., Brandon, R.C., Man-Wai, C.,  
Fitzgerald, L.M., Fitzhugh, M.M., Fitchman, J., Hagedorn, L.D.,  
Glock, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,  
Kellavag, J.M., Kelley, J.C., Liu, L.-I., Karmali, S.M., Kestrick, J.M.,  
Phillips, C.A., Rader, E., Rader, T.R., Rader, T.R., Rader, T.R.,  
Small, K.V., Spisberg, T.A., Uetzel, T.R., Weinstock, K.G.,  
Bednarek, D.P., Celis, E., Fietzmann, R.D., Coleman, A.A., Collins, E.J.,  
He, M., Hu, J.S., Gnehm, J.M., Gnehm, J.M., Gnehm, J.M.,  
Kosak, D.L., Kuo, C.C., Kuo, C.C., Kuo, C.C., Kuo, C.C.,  
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, C.L., Rubin, S.M.,  
Pillon, P.J., Pannon, M.R., Rosen, C.A., Haseltine, M.A., Fields, C.,  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotide cDNA sequence  
9602680

RESULT 16  
LOCUS R66074 354 bp mRNA EST 14-NOV-1995  
DEFINITION Homo sapiens lymph node I Homo sapiens cDNA 5' end similar to  
accession  
Accession R66074  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; Eukaryotes; Eukaryotes; Metazoa; Chordata;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
Hominidae;  
1 (bases 1 to 354)  
REFERENCE  
AUTHORS Hinkle, P.S., Jr., Kellavag, J.M., Kelley, J.C., Liu, L.-I.,  
Karmali, S.M., Kestrick, J.M., Phillips, C.A., Rader, E.,  
Rader, T.R., Rader, T.R., Rader, T.R., Rader, T.R.,  
Small, K.V., Spisberg, T.A., Uetzel, T.R., Weinstock, K.G.,  
Bednarek, D.P., Celis, E., Fietzmann, R.D., Coleman, A.A.,  
Collins, E.J., He, M., Hu, J.S., Gnehm, J.M., Gnehm, J.M.,  
Kosak, D.L., Kuo, C.C., Kuo, C.C., Kuo, C.C., Kuo, C.C.,  
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, C.L., Rubin, S.M.,  
Pillon, P.J., Pannon, M.R., Rosen, C.A., Haseltine, M.A.,  
Fields, C., Initial assessment of human gene diversity and  
expression patterns based upon 83 million nucleotide cDNA  
sequence  
9602680  
TITLE  
JOURNAL MEDLINE  
COMMENT  
Other ESTs: TNC168350  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018509300  
Fax: 3018509305  
Email: arxiv@igrr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Seq primer: M3 Reverse  
Location/Qualifiers  
1. 308  
/organism="Homo sapiens"  
/db\_xref="GeneID:137128"  
/db\_xref="AF001137:137128"  
/clone="11b-Ep1d1yuna"  
/dev="stage=adult"  
/dev="stage=adult"  
BASE COUNT 75 a 107 c 82 g 89 t 1 others  
ORIGIN  
Query Match 3.9% Score 18: DB 16: Length 354:

















**FEATURES**

source  
1. '696  
Location/Qualities 70.  
Seq primer: -40m1 fwd ET from Amerham  
High quality  
Insert Length: 1765 Std Error: 0.00  
found through the I.M.A.C. Consortium/LMBC et  
Cite as: Smith et al., Washington University Genome Sequencing Center  
Cloning Library  
CGMA Library Arraying: Greg Lennon, Ph.D.  
Ph.D. library preparation: Strategene, Inc., David B. Kitzman,  
Emmett-Buck, M.D., Ph.D.

MRNA	176 a	166 c	197 g	157 t
BASE COUNT				
ORIGIN				

```

Query Match Similarity 3.91; Score 18; DB 9; Length 695;
Best Local Similarity 100.00; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 434 ACACCTTCACAGACGCC 431
      |||#####|
Cp 118 ACATCTTCATCTACAGGCC 101

```

[illegible][illegible]

```

Clascom University Genomics Institute
100 Jordan Hall, Clascom University, Clascom, SC 29634
Tel.: 864 555 5737
Fax1: 864 555 4253
Email: jordan@clascom.edu
Seq primer: GGAAGACATGCACTGCACCATC
Class BAC ends
High qual. coverage stop: 439
1..745/Qualifiers

```

A haploid genome (n=7) of approximately 100 Mb. Rice has numerous aspects of the functional potential for studying order to facilitate genome wide analysis, a BAC library BAC was constructed from which an average insert size of 130 kb was obtained. High density colony arrays /40 available upon request.

```

BASE COUNT      213 a      161 c      177 g      189 c      5 others
ORIGIN
Query Match      3.9%; Score 18;  DB 20;  Length 745

```

REFERENCE	TITLE	JOURNAL	COMMENT
1 (pages 1 to 738)			
Hillier, L., Allen, M., Bowles, J., Dubugue, T., Gates, C., Jose, S., Kisman, D., Kucakta, T., Lacy, H., Le, R., Lennon, D., Martin, J., Moore, B., Schellengberg, K., Stephens, J., Zentgraf, T., Zentgraf, T., White, Y., Weller, T., Waterson, R. and Wilson, R.	MeasNoi human ESP Project	Unpublished (1997)	

Contact: Wilson R.  
 444 Washington University School of Medicine  
 660 South Euclid Avenue, Box 8501, St. Louis, MO 63108  
 Tel. 314 286 1800  
 Fax: 314 286 1810  
 Email: wjackson@wustl.edu  
 The following information is available free through LNL; contact the  
 IMAGE Consortium (Amgen/Amgen) for the following information:  
 Seq project: 40M11 fwd. RT from American  
 High quality  
 Locations/analyses: 45.  
 1. 738

[illegible]

```

Query Match      3 9%
Best Local Similarity 100.0%
Matches 18: Conservative
DB 40757 ACCTCTCTCAAGAGGCC 454
CP 118 ACCTCTCTCAAGAGGCC 101

BASE COUNT      181 a 174 c 205 g 178 t

```

```

Apr 19 13:23:57 1999

US-08-036-453-3.25C

Best Local Similarity 100.00;   Pred. No. 1,05e-04;
Matches 16;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
Db      483; GCAGCTGGGCGGTACTCT 498
      72 GCAGCTGGGCGGTACTCT 89

```

[illegible]

FEATURES  
source  
1. 167  
Location/Qualifiers

```

/note/vector: pT7-19ac (Pharmacia) with a modified cDNA  

of the h-h2 gene, site 1, Not I, site 2; Eco RI, at strand  

terminus, site 1, Not I, site 2; Eco RI, at strand  

terminal center, B cells by flow sorting CO2+60,  

provided by Dr. Louis M. Staudt [Mc], Dr. David Allman  

plated with (Not I, oligo dT), h-h2cDNA synthesis was  

15'-TTGATACCTGTAAAGCGAACCACCCGCCCTCATATTTCATTTTATTTT  

[Pharmacia], digested cDNA was ligated to Eco RI adapter  

and Eco RI sites of the modified pT7 vector Library  

can through one round of normalization, and was  

/seq:vector:ca806'

```

Emmett-Buck, M.D., Ph.D.  
Ph.D. Library Preparation: Strategene, Inc., David B. Kitzman,  
CGMA Library Arraying: Greg Lennon, Ph.D.  
Cloning: Center for Genome Sequencing  
Center: Washington University Genome Sequencing Center  
found through the I.M.A.C. Consortium/IMC-cc  
web: bio.lib.gov/bioware/lange.html  
Insert Length: 1765    Std Error: 0.00  
Seq primer: -40m1 fwd    Rr from Amerham  
High quality: 10.  
Location/Qualities:  
1. 696

MRNA	176 a	166 c	197 g	157 t
BASE COUNT				
ORIGIN				

```

Query Match Similarity 3.91; Score 18; DB 9; Length 695;
Best Local Similarity 100.00; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 434 ACACCTTCACAGACGCC 431
      |||#####|
Cp 118 ACATCTTCATCTACAGGCC 101

```

[illegible][illegible]

```

Clascom University Genomics Institute
100 Jordan Hall, Clascom University, Clascom, SC 29634
Tel.: 864 555 5737
Fax1: 864 555 4253
Email: jordan@clascom.edu
Seq primer: GAGACATCATGACATCATCATC
Class BAC ends
High qual. coverage stop: 439
1..745/Qualifiers

```

[illegible]

```

BASE COUNT      213 a      161 c      177 g      189 c      5 others
ORIGIN
Query Match      3.9%; Score 18; DB 20; Length 745

```

REFERENCE	TITLE	JOURNAL	COMMENT
1 (pages 1 to 738)			
Hillier, L., Allen, M., Bowles, L., Dubugue, T., Gates, C., Jose, S., Kisman, D., Kucakta, T., Lacy, H., Le, R., Lennon, D., Mair, B., Martin, J., Moore, B., Schelleng, K., Stephens, J., Thompson, J., Tilling, B., White, Y., Weller, T., Waterson, R. and Wilson, R.	MeasND-NCI human ESP Project	Unpublished (1997)	

Contact: Wilson R.  
 444 Washington University School of Medicine  
 660 South Euclid Avenue, Box 8501, St. Louis, MO 63108  
 Tel. 314 286 1800  
 Fax: 314 286 1810  
 Email: wjackson@wustl.edu  
 The following information is available free through LNL; contact the  
 IMAGE Consortium (Amgen/Amgen) for the following information:  
 Seq project: 40M11 fwd. RT from American  
 High quality  
 Locations/analyses: 45.  
 1. 738

[illegible]

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Query Match      3 9%
Best Local      100.0%
Matches      18: Conservative
DB      118 ACATCTTCACAGAGGCC 454
CP      118 ACATCTTCACAGAGGCC 101

BASE COUNT      181 a 174 c 205 g 178 t

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Apr 19 13:23:57 1999

US-08-036-453-3.rtc

Best Local Similarity 100.00;   Pred. No. 1,05e-04;
Matches 16;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
Db      483; GCACGCTGGGCGCTACACT 498
      07 72 GCACGCTGGGCGCTACACT 89

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ACCESSION	A44386	NCI-CG28
KEYWORDS	NCT059020 059020 BSM PROTEIN; RNA sequence.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryotic mitochondrial eukaryotes; Netacea; Chordata;	
AUTHORS	Kochikubo; Mammalia; Eutheria; Primates; Carnivora; Rodentia;	
TITLE	1 (bases 1 to 167)	
NOTE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgp	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
COMMENT	First index	
	Unpublished (1997)	

FEATURES  
source  
1. 167  
Location/Qualifiers

[illegible]

[illegible]

4444 Forest Park Parkway, Box 5501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
E-mail: wu@slu.edu  
High quality sequence stops: 110  
Source: IMAGE Consortium, LBL  
This clone is available royalty-free through LBL; contact the  
IMAGE Consortium (info@image.lbl.gov) for further information.  
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JOURNAL COMMENT  
 Title Initial Assessment of Human Gene Diversity and Expression Pattern  
 Based Upon 32 Million Basepairs of cDNA Sequence  
 Unpublished (1995)  
 Contact: Venter, JC  
 The Institute for Genomic Research  
 9310 Clopper Rd, Gaithersburg, MD 20878  
 Tel: 3018599431  
 Fax: 3018599432  
 Email: [charlie@edc.tigr.org](mailto:charlie@edc.tigr.org)  
 For clone availability, additional sequence and expression  
 information related to this EST, please contact The TIGR Database  
 (charlie@edc.tigr.org)  
 Location/Qualifiers  
 source 1..209  
 mRNA /organism="Homo sapiens"  
 BASE COUNT 43 a. 52 c 48 g 55 t 1 others  
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 Best Local Similarity 100.0% Prod. No. 43.16  
 Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 150 CGACAGACCGCCGCA 166  
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 Cp 134 CGACAGACCTTCGCA 118  
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 T38670 238 bp 1 mRNA EST 06-SEP-1995  
 T386560 Homo sapiens cDNA 5' end similar to immunoglobulin heavy  
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 ACCESION CHAIN V region  
 MID 9611186  
 KEYWORDS EST  
 SOURCE human, primate-M13 Reverse Library-Human Small Intestine,  
 ORGANISM Eukaryote; Hominidae; Hominidae; Bilateria; Chordata;  
 Vertebrata; Chordata; Vertebrata; Chordata; Chordata;  
 Sarcopterygii; Chondrichthyes; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Artiodactyla; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE Adams M.D., Krawetz S.A.R., Fleischmann R.D., Fuldner R.A.,  
 Bult C.J., Lee N., Kohnen E.F., McIntosh R.C., Gossyne J.D.,  
 White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,  
 Clayton R.D., Cline R.J., Cotton R.D., Eickel-Hugues J., Fink L.D.,

[illegible]



!!SEQUENCE\_LIST 1.0

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FROMIG of: /home/obryen/ee455/olig/us08836455.pep  
sequence 4, application us/08836455

general information:

applicant: chatterjee, malaya

applicant: foon, kenneth a.

applicant: chatterjee, sunil k. . .

TO: geneseqp: \* Sequences: 162,890 Total-Length: 20,225,328 April 18, 1999 14:16

Database Release Information:

Geneseq-AA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

Word-size: 5 Words: 72204 Diagonals: 6,774 Total-Diagonals: 44,984,456

Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 5.18

Sequence Strd Diag Score Width Documentation ..

GENESQOP:W27120	+	0	153--	1	Murine monoclonal anti-idiotypic anti
GENESQOP:P94780	+	0	96	1	2 H7 VH gene. Polynucleotide(s) encod
GENESQOP:W27122	+	-19	96	1	Murine antibody heavy chain variable
GENESQOP:W10588	+	0	96	1	2H7 antibody heavy chain variable reg
GENESQOP:W16343	+	0	96	1	2H7 heavy chain variable sequence. Se
GENESQOP:W10242	+	0	96	1	Heavy chain variable sequence of 2H7.
GENESQOP:W47520	+	0	96	1	Mouse 2H7 antibody heavy chain variab
GENESQOP:W47513	+	0	96	1	Mouse 2H7 antibody heavy chain variab
GENESQOP:W41070	+	0	95	1	Mouse 2H7 antibody heavy chain variab
GENESQOP:P70627	+	0	95	1	Sequence encoded by the 2H7 VH sequen
GENESQOP:R99004	+	0	76	1	Mab VLI765 heavy chain (specific for
GENESQOP:R83111	+	0	74	1	Sequence of murine antibody CC46 VH.
GENESQOP:R55215	+	0	72	1	Murine variable region heavy chain fr
GENESQOP:R62445	+	0	71	1	81C6 heavy chain variable region. Tre
GENESQOP:R04381	+	0	69	1	Variable heavy chain encoded by seq.
GENESQOP:R38310	+	0	69	1	Sequence of VH-alpha-TRG New composi
GENESQOP:W29750	+	0	68	1	Anti-HMFg Mab CTM01 heavy chain varia
GENESQOP:R13061	+	-19	67	2	Monoclonal antibody OK3T heavy chain.
GENESQOP:R15441	+	-19	66	1	Heavy chain variable region of Mab 18
GENESQOP:W27356	+	-19	66	1	Heavy chain variable region of human
GENESQOP:W27359	+	-19	66	1	Heavy chain variable region of chimer
GENESQOP:R79159	+	-19	66	1	Human IGE receptor-binding antibody-2
GENESQOP:R05090	+	0	65	1	Heavy chain variable domain of human
GENESQOP:W19017	+	-20	65	1	Anti-human FasL antibody (NOK5) heavy
GENESQOP:W00831	+	-19	65	2	Variable heavy chain of anti-human Fa
GENESQOP:R79863	+	0	64	1	Anti-EGFR antibody heavy chain variab
GENESQOP:R04384	+	0	64	1	Colon Cancer monoclonal antibody CC83
GENESQOP:R53554	+	0	64	1	DREG-200 Ab heavy chain variable regi
GENESQOP:R38313	+	0	64	1	Sequence of murine antibody CC83 VH.
GENESQOP:W06213	+	0	63	1	Mab Co-1 heavy chain variable region.
GENESQOP:R09425	+	0	63	2	Co-1 Heavy Chain V Region (mouse). CH
GENESQOP:W07436	+	-19	63	2	Anti-DNA antibody 9f11 group heavy ch
GENESQOP:R79865	+	-19	63	1	Anti-EGFR antibody heavy chain variab
GENESQOP:P93151	+	0	62	1	Protein encoded by V and J regions of
GENESQOP:R21884	+	-19	62	1	Murine VH group 1 chain J specific fo
GENESQOP:R21281	+	-19	62	1	Murine VH group 1 chain R specific fo
GENESQOP:R21279	+	-19	62	1	Murine VH group 1 chain P specific fo
GENESQOP:R21274	+	-19	62	1	Murine VH group 1 chain K specific fo
GENESQOP:R21273	+	-19	62	1	Murine VH group 1 chain J specific fo
GENESQOP:R21264	+	-19	62	1	Murine VH group 1 chain A specific fo
GENESQOP:R33950	+	0	62	1	CTM01 VH. Anti-human milk fat globule
GENESQOP:R30014	+	-22	62	1	Heavy chain variable region of anti-P
GENESQOP:R04382	+	2	61	1	Colon Cancer monoclonal antibody CC46
GENESQOP:R04383	+	0	61	1	Colon Cancer monoclonal antibody CC46
GENESQOP:P93079	+	0	61	1	Heavy chain of monoclonal antibody 6A
GENESQOP:R21278	+	-19	61	1	Murine VH group 1 chain O specific fo
GENESQOP:R21276	+	-19	61	1	Murine VH group 1 chain M specific fo
GENESQOP:R38312	+	0	61	1	Sequence of murine antibody CC49 VH.
GENESQOP:W71257	+	0	61	2	Murine antibody ICR-1.1 heavy chain a
GENESQOP:W76127	+	0	61	2	Murine ICR-1.1 V-H region PCR product

*# of seqs containing matches of least 5aa long*

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# MPSRCH

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit,  
Copyright 1993, Biocomputing Research Unit, K.  
Distribution rights by Oxford Molecular Ltd

MPSRCH protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Apr 15 18:12:01 1999; MPSRCH time 5.92 seconds  
Tabular output not generated.  
418,100 Million cell updates/sec

Title: >U8-08-836-455-4  
Description: (1-153) from G8080836455 pep  
Perfect Score: 153  
Sequence: 1 HQSWYPLSLITTCVMSQ.....TVSSNATPPVPLVPMGL 153  
Scoring table: TABLE uniprottable  
Gap 60  
Searched: 131922 seqs, 16180660 residues  
Post-processing: Minimum March 08  
Starting first 1000 summaries

Database: a-geneeq32  
1:part1 2:part3 3:part4 5:part5 6:part6 7:part7  
14:part15 15:part16 16:part17 17:part18 18:part19  
19:part20 20:part21 21:part22 22:part23 23:part24  
24:part25 25:part26 26:part27 27:part28 28:part29  
29:part30  
Statistics: Mean 2.655; Variance 0.895; scale 2.967  
Pred. No. 14: the number of results predicted by chance to have a  
score of 153 or higher is 1.4e-06. This is the probability of  
And is derived by analysis of the total score distribution.

SDMMARIZ

Result		Query		DB	ID	Description	Pred. No.
No.	Score	Match	Length				
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71	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
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73	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
74	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
75	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
76	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
77	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
78	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
79	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
80	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
81	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
82	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
83	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
84	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
85	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
86	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
87	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
88	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
89	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
90	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
91	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
92	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
93	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
94	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
95	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
96	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
97	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06
98	11	447	1	98	114	R21276	Murine VH group 1 cha	4,906-06













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CC antibodies (MEL1, MEL13, MEL15 or MEL17).
Sequence 130 AA:
Query Match 13 43: Score 19; DB 6; Length 130;
Best Local Similarity 100.0%; Pct. No. 1,38e-11;
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 105 dlywgsrctcrvysakttpp 123
|||||
QY 125 dlywgsrctcrvysakttpp 143

RESULT 6
ID R74960 standard: Protein: 133 AA.
AC R74960: 1965 (1484 aa).
CD R74960: 1965 (1484 aa).
DE R74960: 1965 (1484 aa).
KW Antibody; cancer; CDR; heavy chain; immunoglobulin;
NM complementarity determining region.
OS complementarity determining region.
PE Mlu sp.
PT peptide
PT 1 Location/Qualifiers
PT 1..9
PT 101..999 A..
PR 13 OCT-1993: 272950.
PR 06-OCT-1993: 272950.
PR 06-OCT-1993: JP-272950.
PA (HAC1/2) H2AC10KANA T.
PA H2AC10KANA T.
PR N-IPMB 090425.
PR 11 Novel anti-idiotypic antibody against an human anticancer monoclonal
PT antibody, and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
CC R74960-R74965 are clones of the anti-idiotypic antibodies (Id01, Id01017,
CC Id020, Id027 and Id033 against a human anticancer monoclonal antibody
CC Three antibodies and DNA encoding them are useful in pharmacological.
CC These antibodies and DNA encoding them are useful in pharmacological.
Sequence 133 AA:
Query Match 12 43: Score 19; DB 14; Length 133;
Best Local Similarity 100.0%; Pct. No. 1,38e-11;
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 115 dlywgsrctcrvysakttpp 133
|||||
QY 134 dlywgsrctcrvysakttpp 142

RESULT 7
ID R33485 standard: Protein: 134 AA.

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PI  Goultis DB, Kaplan DA, Messa PS, Rixson MH, Schiom J.
PI  WPI: 94-299317/56.
DR  N-PSDB: 071386.
PI  Anti-epitheliomyeloma antigen chimeric antibodies for diagnosis
PI  and treatment of colorectal carcinoma.
PS  Claims 14; Page 53; 67pp; English.
CC  071386 codes for 860566 the antibody heavy chain region of
CC  murine-human anti-epitheliomyeloma antigen (CEA) chimeric
CC  antibody. The antibody is used for diagnosis and treatment of
CC  the detection of CEA, and monitoring of tumor-associated
CC  antigen during therapy. It can also be used in vivo diagnostically,
CC  or in therapy for the treatment of tumors associated with
CC  colorectal and breast carcinoma, as well those of the
CC  gastrointestinal tract, lung, ovary and prostate.
CC  Sequence 114 AA.
50
Query Match 13 41, Score 19; DB 11; Length 124;
Query: 1. Inhibitory 100.0%
Matches 19; Conservative 0; Identical 0; Gaps 0;
DB 4 Jqargqelrvyngsvkmc 22
07 23 LQSGALVYDQSLDQSG 41

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CC specific Ig chains in various organisms provides an effective  
CC solution for the efficient large scale production of human  
CC monoclonal antibodies. The invention also provides a solution to  
CC the problem of class switching antibody molecules.  
SQ Sequence: 140 AA:  
Query Match 12.44: Score 19: DB 29: Length 140:  
Best Local Similarity 100.00: Pred. No. 138e-11:  
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
DB 14 TITVHSDVYDQSSALVIR 32  
QY 14 TITVHSDVYDQSSALVIR 32

RESULT 12  
ID W47513 standard: Protein: 140 AA.  
AC W47513: 1998 (first entry)  
DE 2H7 antibody heavy chain variable region.  
DR 2H7 antibody heavy chain variable region.  
KW Mouse; murine; heavy chain; variable region;  
KW Immunoglobulin fragment production; Ig fragment production;  
KW monoclonal antibody 2H7; human B-cell surface antigen.  
RN 2H7 ap.  
FT Key ap.  
FT Location/Qualifiers  
FT Peptide 1-139  
FT /Label= sig.peptide  
FT /Label= mat.peptide  
FT 20-140  
FT 055698435-A.  
FT 16-DEC-1997.  
FT 06-JUN-1995: 467140.  
FT 01-NOV-1985: US-301982.  
FT 01-NOV-1985: US-301982.  
FT 27-OCT-1986: WO-002289.  
FT 24-JUL-1987: US-077528.  
FT 11-JAN-1988: US-142039.  
FT 01-NOV-1985: US-301982.  
FT 18-DEC-1994: US-390853.  
FT 06-JUN-1995: US-467140.  
FT (XOMA) XOMA CORP.  
FT Better M. Horvitz AH, Lei S, Liu AT, Robinson RR,  
FT N. P808: V18557.  
FT WPI: 98-051492/05.  
FT DR N-P808: V18557.  
FT PT DNA encoding secretable immunoglobulin fragments - comprising at  
FT least one variable region of light or heavy chains  
FT of heavy chain, and a signal sequence for secretion.  
CC The present sequence was used in the development of a novel method  
CC for the production of an immunoglobulin (19) fragment capable of  
CC binding an antigen. The method comprises culturing an E. coli host

FT /Label= FR2  
FT /note= "framework region 2"  
FT region  
FT 69..85  
FT /Label= CDR2  
FT /note= "complementarily determining region 2"  
FT region  
FT 86..117  
FT /Label= FR3  
FT /note= "framework region 3"  
FT region  
FT 118..130  
FT /Label= CDR3  
FT /note= "complementarily determining region 3"  
FT region  
FT 131..140  
FT /Label= FR4  
FT /note= "framework region 4"  
FT 055698435-A.  
FT 16-DEC-1997.  
FT 01-NOV-1985: 793980.  
FT 01-NOV-1985: US-301982.  
FT 27-OCT-1986: WO-002289.  
FT 24-JUL-1987: US-077528.  
FT 11-JAN-1988: US-142039.  
FT 01-NOV-1985: US-301982.  
FT 18-DEC-1994: US-390853.  
FT 06-JUN-1995: US-467140.  
FT (XOMA) XOMA CORP.  
FT Better M. Horvitz AH, Lei S, Liu AT, Robinson RR,  
FT N. P808: V18557.  
FT WPI: 97-225417/20.  
FT DR N-P808: V18557.  
FT PT DNA encoding immunoglobulin heavy and light chain fragments - capable  
FT of assembling into chimeric antibodies, useful for e.g. passive  
FT immunization, diagnosis, etc.  
CC Example 4: Fig 21: 98pp: English.  
CC A human B-cell line secreting the heavy chain variable region of  
CC mouse monoclonal antibody 2H7 which recognizes human B-cell surface  
CC antigen gp35. It is encoded by a cDNA clone (77086) obtained from a  
CC 2H7 cDNA library by PCR amplification. The 2H7 light chain variable  
CC sequence (W47514) is also provided. A novel human-mouse chimeric  
CC antibody molecule is also provided. The 2H7 heavy chain variable  
CC region is specifically for the human B-cell antigen has been  
SQ Sequence: 140 AA:  
Query Match 12.44: Score 19: DB 29: Length 140:  
Best Local Similarity 100.00: Pred. No. 138e-11:  
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CC this has been transformed with a nucleic acid molecule encoding the  
CC heavy chain variable region of human B-cell surface antigen gp35  
CC and secreted. The nucleic acid molecule comprises DNA sequence  
CC encoding: (a) peptide heavy chain variable region operably  
CC linked to a DNA sequence encoding at least the variable region of  
CC an Ig molecule; and (b) peptide light chain variable region of  
CC an Ig molecule operably linked to a DNA sequence encoding at least  
CC the variable region of an Ig molecule. The DNA sequence encoding  
CC to a single polypeptide promoter to form a dicistronic  
CC transcription unit. The method is used to produce chimeric Fab  
CC antibodies. The heavy chain variable region of the human B-cell  
CC antigen gp35 is encoded by a cDNA clone (77086) obtained from a  
CC 2H7 cDNA library by PCR amplification. The 2H7 heavy chain variable  
CC region is specifically for the human B-cell antigen has been  
SQ Sequence: 140 AA:  
Query Match 12.44: Score 19: DB 29: Length 140:  
Best Local Similarity 100.00: Pred. No. 138e-11:  
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 13  
ID W47513 standard: Protein: 140 AA.  
AC W47513: 1998 (first entry)  
DE 2H7 heavy chain variable sequence.  
DR 2H7 heavy chain variable sequence.  
KW Antibody engineering; heavy chain; light chain; chimeric antibody;  
KW 2H7 B-cell antigen gp35.  
RN 2H7 ap.  
FT Key ap.  
FT Location/Qualifiers  
FT Peptide 1-139  
FT /Label= sig.peptide  
FT /Label= mat.peptide  
FT 20-140  
FT 055698435-A.  
FT 16-DEC-1997.  
FT 01-NOV-1985: 793980.  
FT 01-NOV-1985: US-301982.  
FT 27-OCT-1986: WO-002289.  
FT 24-JUL-1987: US-077528.  
FT 11-JAN-1988: US-142039.  
FT 01-NOV-1985: US-301982.  
FT 18-DEC-1994: US-390853.  
FT 06-JUN-1995: US-467140.  
FT (XOMA) XOMA CORP.  
FT Better M. Horvitz AH, Lei S, Liu AT, Robinson RR,  
FT N. P808: V18557.  
FT WPI: 97-225417/20.  
FT DR N-P808: V18557.  
FT PT DNA encoding immunoglobulin fragment - comprising  
FT at least one variable region of light or heavy chains  
FT of heavy chain, and a signal sequence for secretion.  
CC The present sequence was used in the development of a novel method  
CC for the production of an immunoglobulin (19) fragment capable of  
CC binding an antigen. The method comprises culturing an E. coli host

RESULT 14  
ID W47514 standard: Protein: 140 AA.  
AC W47514: 1998 (first entry)  
DE 2H7 antibody heavy chain variable region.  
DR 2H7 antibody heavy chain variable region.  
KW Antibody engineering; heavy chain; light chain; chimeric antibody;  
KW 2H7 B-cell antigen gp35.  
RN 2H7 ap.  
FT Key ap.  
FT Location/Qualifiers  
FT Peptide 1-139  
FT /Label= sig.peptide  
FT /Label= mat.peptide  
FT 20-140  
FT 055698435-A.  
FT 16-DEC-1997.  
FT 01-NOV-1985: 793980.  
FT 01-NOV-1985: US-301982.  
FT 27-OCT-1986: WO-002289.  
FT 24-JUL-1987: US-077528.  
FT 11-JAN-1988: US-142039.  
FT 01-NOV-1985: US-301982.  
FT 18-DEC-1994: US-390853.  
FT 06-JUN-1995: US-467140.  
FT (XOMA) XOMA CORP.  
FT Better M. Horvitz AH, Lei S, Liu AT, Robinson RR,  
FT N. P808: V18557.  
FT WPI: 97-225417/20.  
FT DR N-P808: V18557.  
FT PT DNA encoding immunoglobulin fragment - comprising  
FT at least one variable region of light or heavy chains  
FT of heavy chain, and a signal sequence for secretion.  
CC The present sequence was used in the development of a novel method  
CC for the production of an immunoglobulin (19) fragment capable of  
CC binding an antigen. The method comprises culturing an E. coli host







RESULT	21
ID	M01152 standard; Protein: 162 AA.
NC	M01152:
DE	NB-DE-987 (first entry)
DE	MH1 antibody against heavy chain.
DE	CNR1, light chain: immunoreactive; thrombotic event.
RN	gemifene animal: immunoreactive; thrombotic event.
OS	kiss muscular.
FT	key
FT	domain
FT	domain
FT	domain
FT	domain
FT	domain
PN	M06640986.A1.
PD	19 DEC-1996.
PF	39 APR-1995: D07891.
PR	07-JUN-1995: D5-486420.
PT	DATABASE: AMERICAN BIOGENETIC SCI INC.
P1	DATABASE: AMERICAN BIOGENETIC SCI INC.
DR	MPI: 97-053160/05
DR	N-P508: 759339.
P7	Calibrator comprising lyophilized compn contg. Desmabs fibrin
P7	polymers, buffer and stabilizing agent - for use in soluble fibrin
P7	assays for evaluating pre-disposition to thrombotic event
P3	Disclosed are methods for evaluating pre-disposition to thrombotic event
CC	The present sequence represents English, monoclonal antibody heavy
CC	chain, which was produced in antigen free (germline) mice.
CC	Invention contemplates the production and use of recombinantly producing
CC	portions of, monoclonal antibody MH1 and fusion proteins comprising
CC	antibody NHI, such as oligo peptides including proteins comprising
CC	the antigen binding site of monoclonal antibodies containing
CC	use in as in vitro assay for detecting the presence of calibrator for
CC	crosslinked and soluble non-crosslinked Desmabs fibrin polymers as
CC	specifically binded to calibrator can be used in kits which use an antibody that
CC	antibody. This calibrator is useful in recognizing the NHI monoclonal
CC	thrombotic event, supporting a diagnosis of an occurrence
CC	in storage in the inhibitor exhibits excellent immunoreactive stability
CC	Sequence 162 AA, lyophilized state and after reconstruction.

Query Match	12.4%	Score 19	DB 23	Length 162
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AC W15933:      (first entry)
DT 09-DEC-1987   Antibody G612 heavy chain variable region.
ID K01901        Antibody G612 heavy chain variable region.
KW ZMA012: AA01  Enantioselective hydrolysis; hydroloma;
OS Mus.
PI MO6292426.AL
PI 17-MAR-1986
PI 17-MAR-1986    J00462
PI 17-MAR-1995: NO-020462
(Prot.) PROTEIN ENG RES INSTR.
P1 Fujii T., Kinoshita K., Tanaka F.;
P2 Nishimura M.;
P3 Nishimura M.;
P4 Nishimura M.;
P5 Catalytic antibody for antienantioselective hydrolysis of amino acid esters - also new hydrolomas secreting the antibody
PR Discovered Page 31,32, 49pp; Japanese Patent document no. 56-100000
CC acid catalyzed and the esterified. Preferably the esters are 4-nitro-
CC benzyl esters and the substrates are aromatic amine derivatives.
CC Also disclosed are new hydrolomas expressing the amino-protected,
CC especially ZMA012 (PEW JP-4847) and ZA032 (PEW JP-4846). The
CC (4-carboxy are related in mice using the compound p-nitrobenzoyl-
CC L-alanine as substrate.
CC They are used for efficient asymmetric synthesis of chiral amino acids with
CC high optical selectivity, giving optically active amino acids which
CC are useful for the production of optically active drugs and chiral separation
CC reagents.
CC The present sequence represents the variable region of the heavy chain
CC of antibody G612, produced by the hydroloma ZMA012.
SQ Sequence 212 MA:
Query Match          12 4% Score 19; DB 24; Length 212;
Best Local Similarity 100.00; Pval No. 1.38e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 96 dhwgscvrvtyvaasatctpp 114
Oy 125 dhwgscvrvtyvaasatctpp 143
RESULT: 24
AC W15933: standard Protein: 222 AA.
AC W15934: standard Protein: 222 AA.
D7 09-DEC-1987 (first entry)
DE Antibody 3c2 heavy chain variable region.
ID K01901        Antibody 3c2 heavy chain variable region.
KW ZMA012: AA01  Enantioselective hydrolysis; hydroloma;
OS Mus.
PI MO6292426.AL
PI 26-SEP-1986.

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Matches	19; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
Dd	105 dyvqgsivtvsaahtpp	123			
QY	125 dywqgsivtvsaahtpp	143			

ID	R77306 standard; peptide; 170 AA
AC	R77306

DE CDNA  
KM Humanised antibody; TM29; T cell; Crohn's disease.  
OS Synthetic.

PF 21-JUN-1993.  
 PR 08-NOV-1994; 1B0387.  
 PA (HERC/ MERCER C P.  
 PA (TCEL-) T CELL SCI INC.  
 PI LBN AY;  
 DR WET; 95-224322/39.

PT useful for treatment of Crohn's disease and Multiple Sclerosis  
P5 Disclosure: Page 627, 929p. English  
CC A mouse, monoclonal antibody (mab), 160s, which recognizes human  
CC Fc $\gamma$ R 1, was humanized by CDR grafting certain CDR and select  
CC R1 light chain framework to the murine mab into KOL heavy chain and  
CC heavy (IgG1) and Light (X) chains.  
CC vectors with Neo and DHR-3 chesma hamster fibroblast (CHO) cell  
CC transected into a DHR-3 chesma hamster fibroblast (CHO) cell  
CC recovered by selection and amplification. The humanized mab that  
CC CC R1 beta 8.1.1, it is used to maintain the specificity for human  
CC Crohn's disease.  
SQ Sequence: 110 AA.

50 Sequence 170 AA;

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      12.4%; Score 19; DB 13; Length 170
Best Local Similarity 100.0%; Pred. No. 1.38e-11;

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conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID M15932 standard; Protein; 212 AA

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[illegible]



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FT /label= VH
FT /note= "from MA-15C5"
FT region 100..104
FT /label= VL_anchor_region
FT region 118..122
FT /label= Lab
FT misc_difference 108
FT /note= "mutation v.r.t. original sequence"
PD 31-OCT-1991.
PD MOJ16353-A.
PF 21-APR-1991. E00767.
PR 21-APR-1990. EP-401090.
PI Laroche Y. Holvoet P. Demayer M.
PI WPI: 91-339763/46.
PI New single-chain MAb specific to esp. fibrin - used for imaging,
PI and when connected to plasminogen activating portion used for
PI lysate of thrombi.
PS Disclosure: Fig 6; 78pp: English.
PS A235-8235 may be omitted. The SCa can be labelled and used for the
PS imaging of thrombi. The SCa may be connected, via a 2nd linker
PS catalytic domain of t-pa-activating portion (PA-portion), pref. a
PS thrombolytic agent (SCAP). The SCAP has an increased half-life
PS and has a lower mol.wt. than similar agents and is therefore
PS expected to have a reduced immunogenicity and improved thrombus
PS See also Q14468-70 and R14694-703 and R15690-93.
SQ Sequence 235 AA:
Query Match
Best Local Similarity 100.0% Pred. No. 1386-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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DB 216 dyggsgtvtvysakttpp 234
OY 125 DYGGSGTVTVYSAKTTTP 143
RESULT 30
ID R15690 standard: Protein: 236 AA.
AC R15690:
DT 01-FEB-1992 (first entry)
DR V. Lab-VN construction (4A), single chain antibody.
DS SCa, SCAP, thrombus; t-pa; urokinase.
OS Synthetic.
FH Key
FT region 1..108
FT /label= VL
FT /note= "mutation v.r.t. original sequence"
```

```
OS Synthetic.
FH Key
FT region 1..108
FT /label= VL
FT /note= "mutation v.r.t. original sequence"
FT region 109..117
FT /label= Lab
FT region 118..237
FT /label= VH
FT region 100..104
FT /label= VL_anchor_region
FT region 120..124
FT /label= VL_anchor_region
FT misc_difference 108
FT /note= "mutation v.r.t. original sequence"
FT misc_difference 108
FT /note= "mutation v.r.t. original sequence"
PD 31-OCT-1991.
PD MOJ16353-A.
PF 21-APR-1991. E00767.
PR 21-APR-1990. EP-401090.
PI Laroche Y. Holvoet P. Demayer M.
PI WPI: 91-339763/46.
PI New single-chain MAb specific to esp. fibrin - used for imaging,
PI and when connected to plasminogen activating portion used for
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```
PI lysate of thrombi.
PS Disclosure: Fig 6; 78pp: English.
PS A231-8237 may be omitted. The SCa can be labelled and used for the
PS imaging of thrombi. The SCa may be connected, via a 2nd linker
PS catalytic domain of t-pa-activating portion (PA-portion), pref. a
PS thrombolytic agent (SCAP). The SCAP has an increased half-life
PS and has a lower mol.wt. than similar agents and is therefore
PS expected to have a reduced immunogenicity and improved thrombus
PS See also Q14468-70 and R14694-703 and R15690-93.
SQ Sequence 237 AA:
Query Match
Best Local Similarity 100.0% Pred. No. 1386-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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DB 218 dyggsgtvtvysakttpp 236
OY 125 DYGGSGTVTVYSAKTTTP 143
RESULT 32
ID R15692 standard: Protein: 238 AA.
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FT /note= "from MA-15C5"
FT region 109..116
FT /label= Lab
FT region 117..236
FT /label= VH
FT misc_difference 108
FT /note= "from MA-15C5"
PD 31-OCT-1991.
PD MOJ16353-A.
PF 21-APR-1991. E00767.
PR 21-APR-1990. EP-401090.
PI Laroche Y. Holvoet P. Demayer M.
PI WPI: 91-339763/46.
PI New single-chain MAb specific to esp. fibrin - used for imaging,
PI and when connected to plasminogen activating portion used for
PI lysate of thrombi.
PS Disclosure: Fig 6; 78pp: English.
PS A230-8236 may be omitted. The SCa can be labelled and used for the
PS imaging of thrombi. The SCa may be connected, via a 2nd linker
PS catalytic domain of t-pa-activating portion (PA-portion), pref. a
PS thrombolytic agent (SCAP). The SCAP has an increased half-life
PS and has a lower mol.wt. than similar agents and is therefore
PS expected to have a reduced immunogenicity and improved thrombus
PS See also Q14468-70 and R14694-703 and R15690-93.
SQ Sequence 236 AA:
Query Match
Best Local Similarity 100.0% Pred. No. 1386-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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DB 217 dyggsgtvtvysakttpp 235
OY 125 DYGGSGTVTVYSAKTTTP 143
RESULT 31
ID R15691 standard: Protein: 237 AA.
AC R15691:
DT 01-FEB-1992 (first entry)
DR V. Lab-VN construction (4A), single chain antibody.
DS SCa, SCAP, thrombus; t-pa; urokinase.
OS Synthetic.
FH Key
FT region 1..108
FT /label= VL
FT /note= "mutation v.r.t. original sequence"
FT region 109..116
FT /label= Lab
FT region 117..238
FT /label= VH
FT region 100..104
FT /label= VL_anchor_region
FT region 121..125
FT /label= VL_anchor_region
FT misc_difference 108
FT /note= "mutation v.r.t. original sequence"
FT misc_difference 108
FT /note= "mutation v.r.t. original sequence"
PD 31-OCT-1991.
PD MOJ16353-A.
PF 21-APR-1991. E00767.
PR 21-APR-1990. EP-401090.
PI Laroche Y. Holvoet P. Demayer M.
PI WPI: 91-339763/46.
PI New single-chain MAb specific to esp. fibrin - used for imaging,
PI and when connected to plasminogen activating portion used for
```

```
PI lysate of thrombi.
PS Disclosure: Fig 6; 78pp: English.
PS A231-8237 may be omitted. The SCa can be labelled and used for the
PS imaging of thrombi. The SCa may be connected, via a 2nd linker
PS catalytic domain of t-pa-activating portion (PA-portion), pref. a
PS thrombolytic agent (SCAP). The SCAP has an increased half-life
PS and has a lower mol.wt. than similar agents and is therefore
PS expected to have a reduced immunogenicity and improved thrombus
PS See also Q14468-70 and R14694-703 and R15690-93.
SQ Sequence 238 AA:
Query Match
Best Local Similarity 100.0% Pred. No. 1386-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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DB 219 dyggsgtvtvysakttpp 237
OY 125 DYGGSGTVTVYSAKTTTP 143
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RESULT 33  
ID R16593 standard: Protein: 239 AA.  
DE 01-FEB-1992 (first entry)  
DE V1-Lab-VH construction (4A), single chain antibody.  
KW SCA: SCAPA, trombus, t-PA, urokinase.  
OS Synthetic.  
FT region location/Qualifiers  
FT 1-108 /label=V1  
FT 109-119 /note="from MA-15C5"  
FT 120-239 /label=Vh  
FT 120-239 /note="from MA-15C5"  
FT 121-126 /label=Vh  
FT 121-126 /label=Vh\_anchor\_region  
FT 121-126 /note="mutation v.r.t. original sequence"  
FT misc\_difference 108 /note="mutation v.r.t. original sequence"  
FT W01163531-N.  
PD 21-OCT-1991 P00767  
PR 23-APR-1990: EP-401090.  
PA (CORV-) CORVAS INT NW.  
PI Laroche Y, Holyst P, Demayer M;  
PM 91-13578/46: this specific to epp. fibrin - used for imaging,  
PT and when connected to plasminogen activating portion used for  
PT lysate of thrombi.  
PS Disclosure: Fig 6; 78pp: English.  
CC 121-553 may be omitted. The SCA can be labelled and used for the  
CC imaging of thrombi. The SCA may be connected v.t. 2nd fibrin  
CC (led) to a plasminogen activating portion (PA-portion), pref. a  
CC catalytic domain of t-PA or urokinase, esp. scupA, to form a  
CC thrombolytic agent (SCAPA). The SCAPA has an increased half-life  
CC and a lower mol. wt. than fibrinolytic agents and is therefore  
CC expected to have a reduced immunogenicity and improved thrombus  
CC penetration.  
CC See also Q14466-70 and R14694-703 and R15690-93.  
SQ Sequence 239 AA:  
Query Match 12.4% Score 19: DB 3: Length 239:  
Best Local Similarity 100.0% Pred. No. 1.38e-11:  
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 35  
ID R76085 standard: Peptide: 445 AA.  
DE 02-SEP-1986 (first entry)  
DE MAB 55.1 heavy chain.  
KW Antigen binding structure: complementary determining region; CDR;  
KW CASS.1; colorectal cancer; tumor-associated antigen; hybridoma;  
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;  
KW humanized antibody; immunotoxin.  
OS Mus sp.  
PN M0515382-N.  
PD 28-NOV-1984 G03610  
PR 03-DEC-1993: DB-024619.  
PA 03-JUN-1994: DB-011089.  
PI (28NE) GENEXA LTD. Coplay CO, Wall SW, Paterson DS;  
PM Rose NS, Wright AF;  
PT WPI: 95-215262/28.  
PS Antigen binding structures containing CDRs recognizing the CASS.1  
PS antigen, produced by hybridoma and host cells, for use in the  
PS treatment of colorectal cancer. English.  
CC Chain 3: Page 97-98, 121pp: English.  
CC An antigen binding structure is based on the CDRs (given in R76078-  
CC 84) of the heavy (R76085) and light (R76086) chains of MAb 55.1  
CC (CDACC 354101). This structure recognizes the colorectal tumor-associated  
CC antigen CASS.1. It is expected that this structure will be useful in  
CC (Fab'), Fab', Fv, scFv or V-chain, and is produced in transgenic  
CC animals or plants.  
SQ Sequence 445 AA:  
Query Match 12.4% Score 19: DB 13: Length 445:  
Best Local Similarity 100.0% Pred. No. 1.38e-11:  
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 36  
ID R39643 standard: Protein: 448 AA.  
AC R39643  
DE 11-OCT-1996 (first entry)  
DE Anti-bovine growth hormone heavy chain.  
KW Antibody engineering: single polypeptide chain binding molecule;  
KW heavy chain; light chain; monoclonal antibody; MAb;  
KW bovine growth hormone; bGH; immunoreactivity purification.

DB 220 dywgggtrvysakttpp 238  
QY 125 DYWGQGSYVYSNAKTPP 143  
RESULT 34  
ID R14698 standard: Protein: 243 AA.  
DE 01-FEB-1992 (first entry)  
DE V1-Lab-VH construction (4A), single chain antibody.  
KW SCA: SCAPA, trombus, t-PA, urokinase.  
OS Synthetic.  
FT region location/Qualifiers  
FT 1-108 /label=V1  
FT 109-119 /note="from MA-15C5"  
FT 120-239 /label=Vh  
FT 120-239 /note="from MA-15C5"  
FT 121-126 /label=Vh  
FT 121-126 /label=Vh\_anchor\_region  
FT 121-126 /note="mutation v.r.t. original sequence"  
FT W01163531-N.  
PD 21-OCT-1991 P00767  
PR 23-APR-1990: EP-401090.  
PA (CORV-) CORVAS INT NW.  
PI Laroche Y, Holyst P, Demayer M;  
PM 91-13578/46: this specific to epp. fibrin - used for imaging,  
PT and when connected to plasminogen activating portion used for  
PT lysate of thrombi.  
PS Disclosure: Fig 6; 78pp: English.  
CC 121-553 may be omitted. The SCA can be labelled and used for the  
CC imaging of thrombi. The SCA may be connected v.t. 2nd fibrin  
CC (led) to a plasminogen activating portion (PA-portion), pref. a  
CC catalytic domain of t-PA or urokinase, esp. scupA, to form a  
CC thrombolytic agent (SCAPA). The SCAPA has an increased half-life  
CC and a lower mol. wt. than fibrinolytic agents and is therefore  
CC expected to have a reduced immunogenicity and improved thrombus  
CC penetration.  
CC See also Q14466-70 and R14694-703 and R15690-93.  
SQ Sequence 243 AA:  
Query Match 12.4% Score 19: DB 3: Length 243:  
Best Local Similarity 100.0% Pred. No. 1.38e-11:  
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OS Mus sp.  
PN M0515382-N.  
PD 28-NOV-1984 G03610  
PR 02-SEP-1986: DB-902971.  
PR 02-SEP-1986: DB-902971.  
PR 13-NOV-1989: DB-396417.  
PR 25-APR-1990: DB-512910.  
PR 01-APR-1993: DB-040440.  
PR 06-JUN-1995: DB-468992.  
PA (28NE) GENEXA LTD. Coplay CO, Wall SW, Paterson DS;  
PM Rose NS, Wright AF;  
PT WPI: 95-215262/28.  
PS Antigen binding structures containing CDRs recognizing the CASS.1  
PS antigen, produced by hybridoma and host cells, for use in the  
PS treatment of colorectal cancer. English.  
CC Chain 3: Page 97-98, 121pp: English.  
CC An antigen binding structure is based on the CDRs (given in R76078-  
CC 84) of the heavy (R76085) and light (R76086) chains of MAb 55.1  
CC (CDACC 354101). This structure recognizes the colorectal tumor-associated  
CC antigen CASS.1. It is expected that this structure will be useful in  
CC (Fab'), Fab', Fv, scFv or V-chain, and is produced in transgenic  
CC animals or plants.  
SQ Sequence 448 AA:  
Query Match 12.4% Score 19: DB 18: Length 448:  
Best Local Similarity 100.0% Pred. No. 1.38e-11:  
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 37  
ID R43673 standard: Protein: 448 AA.  
AC R43673  
DE 23-APR-1990 (first entry)  
DE Mouse anti-bovine growth hormone MAb heavy chain.  
KW Monoclonal antibody; MAb; affinity: binding; antigen: diagnostics;  
KW therapy; imaging; purification; biosensors.  
PN 085200203-N.  
PD 09-NOV-1993.  
PF 02-SEP-1986: 902971.









!!SEQUENCE LIST 1.0  
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FROM: of: /home/obryen/ree455/olig/US08836455.pep  
sequence 4, application us/08836455

general information:  
applicant: chatterjee, malaya  
applicant: toon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: pir: \* Sequences: 116,738 Total-length: 37,460,341 April 18, 1999 19:16

Database Release Information:

NBRF, Release 58.0, Released on 30Sep1998, Formatted on 15Dec1998

Word-size: 5 Words: 56967 Diagonals: 6,675 Total-diagonals: 55,204,517  
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 4.59

Sequence Strd Diag Score Width Documentation ..

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PIR2:S42177	-26	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42181	-26	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42176	-26	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42184	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42179	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42180	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:S25057	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:H32513	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:PH1000	-19	67	1	Ig heavy chain precursor V region (B)
PIR2:S41394	-19	67	1	Ig heavy chain V region (clone 202.10
PIR1:HVM502	-19	66	1	Ig heavy chain V region - mouse
PIR2:S37201	-19	65	1	Ig heavy chain precursor V region (10
PIR1:HVM507	-19	64	1	Ig heavy chain precursor V region (9)
PIR2:PH1494	-19	64	1	Ig heavy chain V region (clones X7-3d1
PIR2:PH1484	-19	64	1	Ig heavy chain V region (clones X7-3d
PIR2:PH1482	-19	64	1	Ig heavy chain V region (clones 36-35
PIR2:S38717	-19	64	1	Ig heavy chain V region - mouse
PIR2:PH1486	-19	63	1	Ig heavy chain V region (clone X7-3d1
PIR2:A27609	-19	63	1	Ig heavy chain precursor V region (12
PIR2:PI10247	-22	63	1	Ig heavy chain V region (anti-DNA, 11
PIR2:A39276	-22	63	1	Ig heavy chain precursor V-D-J region
PIR2:S21810	-13	62	1	Ig heavy chain V region - mouse
PIR2:PH1512	-13	62	1	Ig heavy chain V region (clone X7-5D3
PIR2:PH1498	-13	62	1	Ig heavy chain V region (clone X7-4G7
PIR2:PH1001	-19	62	1	Ig heavy chain V region (clone 111.66
PIR2:S20643	-19	62	1	Ig heavy chain V region - mouse
PIR2:A54378	-19	62	1	Ig heavy chain V region anti-triplex
PIR1:HVM584	-19	61	1	Ig heavy chain precursor V region (10
PIR2:PS0024	-19	61	1	Ig heavy chain precursor V region (6)
PIR2:PH1005	-19	61	1	Ig heavy chain V region (clone 202.54
PIR2:S38950	-19	61	1	Ig gamma chain - mouse
PIR2:S40295	-19	61	2	Ig gamma-2a chain (mb735) - mouse
PIR2:S53751	-19	61	1	antibody Fab Jcl 103 heavy chain - mc
PIR2:B22769	-19	61	1	Ig heavy chain V region (B1-8.V1/V2)
PIR2:PC1155	-19	59	1	Ig heavy chain precursor V region (B7
PIR2:PH1502	-13	59	1	Ig heavy chain V region (clone X7-5D3
PIR2:PH1493	-13	59	1	Ig heavy chain V region (clone PR14-3
PIR2:PH0998	-19	59	1	Ig heavy chain V region (clone 165.3)
PIR2:PH1492	-19	59	1	Ig heavy chain V region (clone PR11-4
PIR2:S01321	-19	59	1	Ig gamma-2b chain precursor - mouse
PIR2:S55541	-19	59	1	Ig heavy chain V region (clone X41-2)
PIR2:PH1500	-13	58	1	Ig heavy chain V region (clone X7-5D3
PIR2:PH1489	-13	58	1	Ig heavy chain V region (clones X7-5
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PIR2:PH1522	-13	58	1	Ig heavy chain V region (clone PR14-3
PIR2:PH1521	-13	58	1	Ig heavy chain V region (clone X41-32
PIR2:PH0989	-19	58	1	Ig heavy chain V region - mouse (frag
PIR2:PH0997	-19	58	1	Ig heavy chain V region (clone 17s-c2
PIR2:PH0995	-19	58	1	Ig heavy chain V region (clone 202.61

*not all of these containing matches at least 5 aa long*

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971 6 3 9 349 3 36311 (interferon receptor-c 1,15e+02  
972 6 3 9 359 2 B1566 beta-2-microglobulin 1,15e+02  
973 6 3 9 360 2 S26241 beta-2-microglobulin 1,15e+02  
974 6 3 9 364 2 C48376 mcd protein - tescher 1,15e+02  
975 6 3 9 403 2 B25058 probable viral protein 1,15e+02  
976 6 3 9 407 2 A72993 epolipoprotein A-I re 1,15e+02  
977 6 3 9 412 2 I48975 epolipoprotein A-I re 1,15e+02  
978 6 3 9 413 2 A71333 hemoglobin homolog pro 1,15e+02  
979 6 3 9 423 1 C47714 conserved hypoxanthine 1,15e+02  
980 6 3 9 438 2 C46554 hypothetical 51.6k pr 1,15e+02  
981 6 3 9 440 2 A12509 probable transcrip 1,15e+02  
982 6 3 9 507 2 A12509 poly A polymerase 1,15e+02  
983 6 3 9 513 2 C70485 sperm surface protein 1,15e+02  
984 6 3 9 529 2 A36343 neuroglycan C precursor 1,15e+02  
985 6 3 9 544 2 B14447 neuroglycan C precursor 1,15e+02  
986 6 3 9 544 2 B14447 neuroglycan C precursor 1,15e+02  
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DATE 07-Jun-1992  
ACCESSIONS 1  
AUTHORS 1  
TITLE 1  
STRUCTURAL CHARACTERIZATION OF ANTI-IDIOTYPIC ANTIBODIES;  
DIFFERENTIALLY CHAIN AB2B.  
ACCESSION P10089  
MOLECULE-TYPE mRNA

Mon Apr 19 13:21:59 1999

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Page 23

118-125  
117-151  
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Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 122 GADTGGCGTCTGATGATTP 143

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ORIGINISM 3  
DATE 28-Sep-1992  
ACCESSIONS 3  
AUTHORS 3  
TITLE 3  
STRUCTURAL CHARACTERIZATION OF ANTI-IDIOTYPIC ANTIBODIES;  
DIFFERENTIALLY CHAIN AB2B.  
ACCESSION P10089  
MOLECULE-TYPE mRNA

RESULT 4  
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ACCESSIONS 4  
AUTHORS 4  
TITLE 4  
STRUCTURAL CHARACTERIZATION OF ANTI-IDIOTYPIC ANTIBODIES;  
DIFFERENTIALLY CHAIN AB2B.  
ACCESSION P10089  
MOLECULE-TYPE mRNA

Mon Apr 19 13:21:59 1999

US-08-836-455-4.FP2

Page 22

971 6 3 9 349 3 36311 (interferon receptor-c 1,15e+02  
972 6 3 9 359 2 B1566 beta-2-microglobulin 1,15e+02  
973 6 3 9 360 2 S26241 beta-2-microglobulin 1,15e+02  
974 6 3 9 364 2 C48376 mcd protein - tescher 1,15e+02  
975 6 3 9 403 2 B25058 probable viral protein 1,15e+02  
976 6 3 9 407 2 A72993 epolipoprotein A-I re 1,15e+02  
977 6 3 9 412 2 I48975 epolipoprotein A-I re 1,15e+02  
978 6 3 9 413 2 A71333 hemoglobin homolog pro 1,15e+02  
979 6 3 9 423 1 C47714 conserved hypoxanthine 1,15e+02  
980 6 3 9 438 2 C46554 hypothetical 51.6k pr 1,15e+02  
981 6 3 9 440 2 A12509 probable transcrip 1,15e+02  
982 6 3 9 507 2 A12509 poly A polymerase 1,15e+02  
983 6 3 9 513 2 C70485 sperm surface protein 1,15e+02  
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Mon Apr 19 13:21:59 1999

US-08-836-455-4.FP2

Page 24

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ACCESSIONS 5  
AUTHORS 5  
TITLE 5  
STRUCTURAL CHARACTERIZATION OF ANTI-IDIOTYPIC ANTIBODIES;  
DIFFERENTIALLY CHAIN AB2B.  
ACCESSION P10089  
MOLECULE-TYPE mRNA





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AUTHOR     06-Jan-1995 sequence accession name house mouse
DATE       08-Sep-1997
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KEYWORDS   Kabat, J.
SUBMISSION submission submitted to the EMBL Data Library, April 1991
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Best Local Similarity 100.0% Pval 0.67721 Indels 0 Gaps 0:
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DB 84 SELESTASYPCABH 100
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TITLE      1 gamma chain - mouse
AUTHOR     formal name Mus musculus common_name house mouse
DATE       12-May-1994 sequence revision 10-Nov-1995 text change
          S38950
ACCESSIONS S38950
REFERENCE   Kiezin, S.; Kravitz, H.D.; Zimmermann, B.; Vaseen, M.;
           Froese, M.; Weisberger, C.; Bitter-Suermann, D.:
           Biol. Chem. Hoppe-Seyler (1993) 374:993-1000
           Primary structure of the murine monoclonal IgG2c antibody
           mAb35 against alpha(2-8) polysialic acid. ? Amino acid
           sequence of the heavy (H)-chain Pd region.
           S38950
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            strandness 1..46 #label KIEZ
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KEYWORD     immunoglobulin

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 REFERENCE 509216  
 #journal Okamoto, M.; Hori, T.  
 #title Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoantibody produced by a hybridoma from NZB  
 #cross-reference MWID:90245589  
 #accession 509216  
 #status preliminary  
 #molecule\_type RNA  
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 #cross-reference EMBL:K1741  
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 #molecule\_type RNA  
 #status preliminary  
 #residues 1-43  
 #keywords 1-43  
 #cross-reference 1-43  
 CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY 4412  
 #length 43 checksum 4412

#journal D. J. Marfaty-Bostein, A.; Wiegert, M.  
 #title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.  
 #cross-reference EMBL:9011618  
 #accession P10242  
 #molecule\_type RNA  
 #residues 1-91  
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 FEATURE heterotrimer; immunoglobulin  
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 #region complementarity-determining 1  
 #region framework 2  
 #region complementarity-determining 2  
 #region framework 3  
 #region complementarity-determining 3  
 #region framework 4  
 #region framework 5  
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 #cross-reference 1-91  
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 SUMMARY 1284  
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 QY 103 SSTSDESAVPCAR 117  
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 #cross-reference 1-43  
 CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
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 QY 103 SSTSDESAVPCAR 117  
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 QY 103 SSTSDESAVPCAR 117  
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 SUMMARY 121  
 #length 94 checksum 121  
 Query Match 9.84: Score 15; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2,736-16;  
 Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 63 SSTSDESAVPCAR 77  
 QY 103 SSTSDESAVPCAR 117  
 #accession 511111  
 #molecule\_type RNA  
 #status preliminary  
 #residues 1-96  
 #keywords 1-96  
 #cross-reference 1-96  
 CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY 121  
 #length 96 checksum 121  
 Query Match 9.84: Score 15; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 2,736-16;  
 Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 63 SSTSDESAVPCAR 77  
 QY 103 SSTSDESAVPCAR 117  
 #accession 511111  
 #molecule\_type RNA  
 #status preliminary  
 #residues 1-96  
 #keywords 1-96  
 #cross-reference 1-96  
 CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
 SUMMARY 121  
 #length 96 checksum 121

```

#authors TILMAN, D.M.; SHAN, N.T.; HILL, R.J.; MARION, T.N.
#journal J. Exp. Med. (1992) 176:161-176
#title Both IgM and IgG anti-DNA antibodies are the products of
#         clonally selective B cell stimulation in (NZB x NZW)F1
#         mice.
#accession PH1000
#molecule_type mRNA
#residues 1-106
#sequence 1-106
#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 15-97 $domain immunoglobulin homology $label IMM
Query Match 9.84; Score 15; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 83 SSTSDBAVTCAR 97
OY 103 SSTSDBAVTCAR 117

RESULT 30
ENTRY PH10240
TITLE Ig heavy chain V region (anti-DNA, 537YR) - mouse (fragment)
ORIGINISM $formal_name Mus musculus $common_name house mouse
DATE 16-Sep-1992 $sequence_revision 16-Sep-1992 $text_change
ACCESSIONS PH10240
REFERENCES SHIMOMURA, K.; MARCELLI, M.; SHAN, N.T.; RADIC, M.Z.; PIETAKY,
#authors J. Exp. Med. (1990) 171:265-287
#journal Anti-DNA antibodies from autoimmune mice arise by clonal
#         expansion and somatic mutation.
#accession PH10240
#molecule_type mRNA
#residues 1-107
#sequence 1-107
#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 1-18 $region framework 1\
3-86 $domain immunoglobulin homology $label IMM
19-23 $region complementarity-determining 1\
38-54 $region complementarity-determining 2\
55-86 $region framework 3\
Query Match 9.84; Score 15; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 72 SSTSDBAVTCAR 86
OY 103 SSTSDBAVTCAR 117
```

```

RESULT 32
ENTRY PH10316
TITLE Ig heavy chain V region - mouse
ORIGINISM $formal_name Mus musculus $common_name house mouse
DATE 13-Jan-1995 $sequence_revision 13-Jan-1995 $text_change
ACCESSIONS PH10316
REFERENCES STARR, S.E.; CATON, A.J.
#authors J. Exp. Med. (1991) 174:613-624
#journal Antibodies that are specific for a single amino acid
#         epitope on a protein: protein epitope used structurally distinct
#         variable regions.
#accession PH10316
#molecule_type mRNA
#residues 1-108
#sequence 1-108
#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 15-98 $domain immunoglobulin homology $label IMM
Query Match 9.84; Score 15; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 94 ALDWDGCTVTVS 108
OY 133 ALDWDGCTVTVS 137

RESULT 33
ENTRY PH0997
TITLE Ig heavy chain V region (clone 17-c2) - mouse (fragment)
ORIGINISM $formal_name Mus musculus $common_name house mouse
DATE 30-Sep-1992 $sequence_revision 30-Sep-1992 $text_change
ACCESSIONS PH0997
REFERENCES TILMAN, D.M.; SHAN, N.T.; HILL, R.J.; MARION, T.N.
#authors J. Exp. Med. (1992) 176:161-176
#journal Both IgM and IgG anti-DNA antibodies are the products of
#         clonally selective B cell stimulation in (NZB x NZW)F1
#         mice.
#accession PH0997
#molecule_type mRNA
#residues 1-109
#sequence 1-109
#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 15-98 $domain immunoglobulin homology $label IMM
Query Match 9.84; Score 15; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 84 SSTSDBAVTCAR 98
OY 103 SSTSDBAVTCAR 117
```

```

#authors TILMAN, D.M.; SHAN, N.T.; HILL, R.J.; MARION, T.N.
#journal J. Exp. Med. (1992) 176:161-176
#title Both IgM and IgG anti-DNA antibodies are the products of
#         clonally selective B cell stimulation in (NZB x NZW)F1
#         mice.
#accession PH1000
#molecule_type mRNA
#residues 1-110
#sequence 1-110
#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 15-98 $domain immunoglobulin homology $label IMM
Query Match 9.84; Score 15; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 72 SSTSDBAVTCAR 86
OY 103 SSTSDBAVTCAR 117

RESULT 31
ENTRY PH10241
TITLE Ig heavy chain V region (anti-DNA, 541YR) - mouse (fragment)
ORIGINISM $formal_name Mus musculus $common_name house mouse
DATE 16-Aug-1996 $sequence_revision 16-Sep-1992 $text_change
ACCESSIONS PH10241
REFERENCES SHIMOMURA, K.; MARCELLI, M.; SHAN, N.T.; RADIC, M.Z.; PIETAKY,
#authors J. Exp. Med. (1990) 171:265-287
#journal Anti-DNA antibodies from autoimmune mice arise by clonal
#         expansion and somatic mutation.
#accession PH10241
#molecule_type mRNA
#residues 1-107
#sequence 1-107
#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 1-18 $region framework 1\
3-86 $domain immunoglobulin homology $label IMM
19-23 $region complementarity-determining 1\
38-54 $region complementarity-determining 2\
55-86 $region complementarity-determining 3\
58-107 $region framework 4\
Query Match 9.84; Score 15; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 72 SSTSDBAVTCAR 86
OY 103 SSTSDBAVTCAR 117
```

```

#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 15-98 $domain immunoglobulin homology $label IMM
Query Match 9.84; Score 15; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 84 SSTSDBAVTCAR 98
OY 103 SSTSDBAVTCAR 117

RESULT 34
ENTRY PH1000
TITLE Ig heavy chain V region (clone 201.105) - mouse (fragment)
ORIGINISM $formal_name Mus musculus $common_name house mouse
DATE 30-Sep-1992 $sequence_revision 30-Sep-1992 $text_change
ACCESSIONS PH1000
REFERENCES TILMAN, D.M.; SHAN, N.T.; HILL, R.J.; MARION, T.N.
#authors J. Exp. Med. (1992) 176:161-176
#journal Both IgM and IgG anti-DNA antibodies are the products of
#         clonally selective B cell stimulation in (NZB x NZW)F1
#         mice.
#accession PH1000
#molecule_type mRNA
#residues 1-110
#sequence 1-110
#experimental_source B cell, strain [NZB x NZW]F1
#heterotetramer: immunoglobulin
#FEATURES
SDRAW 15-98 $domain immunoglobulin homology $label IMM
Query Match 9.84; Score 15; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 84 SSTSDBAVTCAR 98
OY 103 SSTSDBAVTCAR 117
```

RESULT 36  
ENTRY 36  
TITLE 1g heavy chain V region - mouse (fragment)  
ORIGINISM 19-Mar-1998 sequence\_revision 10-Mar-1998 text\_change  
DATE 17-Apr-1998  
ACCESSIONS 826033  
REFERENCES 826030  
AUTHORS Stark, S.E.; Caton, A.J.  
J. Exp. Med. (1991) 174:613-624  
TITLE Antibodies that are specific for a single amino acid  
antigenic determinant are structurally distinct  
variable regions.  
#molecule-type RNA  
#residues 1-110 #label STR  
#accession EMBL:K67171; NID:950081; PID:444192; PID:9133867  
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SYNOPSIS length 110 checksum 513  
Query Match 9.8% Score 15; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 2,736-16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 96 AIDYMGCGTGYTSS 110  
|||||  
QY 123 AIDYMGCGTGYTSS 137

RESULT 36  
ENTRY 36  
TITLE 1g heavy chain V region (fragment)  
ORIGINISM 19-Mar-1998 sequence\_revision 10-Mar-1998 text\_change  
DATE 17-Apr-1998  
ACCESSIONS 825033  
REFERENCES 825032  
AUTHORS Stark, S.E.; Caton, A.J.  
J. Exp. Med. (1991) 174:613-624  
TITLE Antibodies that are specific for a single amino acid  
antigenic determinant are structurally distinct  
variable regions.  
#molecule-type RNA  
#residues 1-110 #label STR  
#accession EMBL:K67171; NID:950081; PID:444192; PID:9133867  
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SYNOPSIS length 110 checksum 513  
Query Match 9.8% Score 15; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 2,736-16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 96 AIDYMGCGTGYTSS 110  
|||||  
QY 123 AIDYMGCGTGYTSS 137

RESULT 36  
ENTRY 36  
TITLE 1g heavy chain V-D-J region (106-10P) - mouse (fragment)  
ORIGINISM 12-Feb-1993 sequence\_revision 12-Feb-1993 text\_change  
DATE 06-Sep-1997  
ACCESSIONS 509957  
REFERENCES 509955  
AUTHORS Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.  
Eur. J. Immunol. (1990) 20:771-777  
TITLE Variable region sequences of pathogenic anti-mouse red blood  
cell autoantibodies from autoimmune NZB mice  
#accession EMBL:90269378  
#molecule-type RNA  
#residues 1-112 #label RET  
#accession EMBL:K51845; NID:953244; PID:930213  
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SYNOPSIS length 112 checksum 334  
Query Match 9.8% Score 15; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2,736-16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 14 SASVYSCASGCT 28  
|||||  
QY 33 SASVYSCASGCT 47

RESULT 39  
ENTRY 39  
TITLE 1g heavy chain V region pc23 - mouse (fragment)  
ORIGINISM 19-Mar-1998 sequence\_revision 10-Mar-1998 text\_change  
DATE 17-Apr-1998  
ACCESSIONS 855535  
REFERENCES 855528  
AUTHORS Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Exp. Med. (1995) 181:1495-1504  
TITLE Comprehensive epitope analysis of monoclonal  
anti-precipitin antibodies using phage display libraries  
and synthetic peptides: revelation of antibody fine  
structure and identification of somatic mutations in the variable  
region genes.  
#accession EMBL:K55535  
#molecule-type RNA  
#residues 1-111 #label JMW

RESULT 37  
ENTRY 37  
TITLE 1g heavy chain V region pc23 - mouse (fragment)  
ORIGINISM 19-Mar-1998 sequence\_revision 10-Mar-1998 text\_change  
DATE 17-Apr-1998  
ACCESSIONS 855535  
REFERENCES 855528  
AUTHORS Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Exp. Med. (1995) 181:1495-1504  
TITLE Comprehensive epitope analysis of monoclonal  
anti-precipitin antibodies using phage display libraries  
and synthetic peptides: revelation of antibody fine  
structure and identification of somatic mutations in the variable  
region genes.  
#accession EMBL:K55535  
#molecule-type RNA  
#residues 1-111 #label JMW

RESULT 37  
ENTRY 37  
TITLE 1g heavy chain V region pc23 - mouse (fragment)  
ORIGINISM 19-Mar-1998 sequence\_revision 10-Mar-1998 text\_change  
DATE 17-Apr-1998  
ACCESSIONS 855535  
REFERENCES 855528  
AUTHORS Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Exp. Med. (1995) 181:1495-1504  
TITLE Comprehensive epitope analysis of monoclonal  
anti-precipitin antibodies using phage display libraries  
and synthetic peptides: revelation of antibody fine  
structure and identification of somatic mutations in the variable  
region genes.  
#accession EMBL:K55535  
#molecule-type RNA  
#residues 1-111 #label JMW

RESULT 40  
ENTRY 40  
TITLE 1g heavy chain V region anti-triplep DNA - mouse (fragment)  
ORIGINISM 06-Oct-1994 sequence\_revision 16-Nov-1994 text\_change  
DATE 30-May-1997  
ACCESSIONS A54378  
REFERENCES A54376  
AUTHORS Y.M.; Tan, J.S.; Bartholomew, G.D.  
J. Biol. Chem. (1994) 269:1351-1357  
TITLE Characterization of a new monoclonal antibody to triplep DNA  
and immunofluorescent staining of mammalian chromosomes.  
#accession EMBL:9416109  
#molecule-type RNA  
#residues 1-115 #label AGA  
#accession EMBL:K67171; NID:950081; PID:444192; PID:9133867  
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SYNOPSIS length 115 checksum 644

RESULT 40  
ENTRY 40  
TITLE 1g heavy chain V region anti-triplep DNA - mouse (fragment)  
ORIGINISM 06-Oct-1994 sequence\_revision 16-Nov-1994 text\_change  
DATE 30-May-1997  
ACCESSIONS A54378  
REFERENCES A54376  
AUTHORS Y.M.; Tan, J.S.; Bartholomew, G.D.  
J. Biol. Chem. (1994) 269:1351-1357  
TITLE Characterization of a new monoclonal antibody to triplep DNA  
and immunofluorescent staining of mammalian chromosomes.  
#accession EMBL:9416109  
#molecule-type RNA  
#residues 1-115 #label AGA  
#accession EMBL:K67171; NID:950081; PID:444192; PID:9133867  
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology  
KEYWORDS heterotetramer; immunoglobulin  
SYNOPSIS length 115 checksum 644

```
RESULT 41
ENTRY PLO238      type fragment
TITLE Ig heavy chain V region (anti-DNA, 6N9H and 6QVH) - mouse
ORGANISM Mus musculus (common name house mouse)
DATE 16-Sep-1992 sequence_revision 16-Sep-1992 text_change
ACCESSION PLO238
REFERENCE Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plautsky,
          J. Exp. Med. (1990) 171:265-297
          Anti-DNA antibodies from autoimmune mice arise by clonal
          expansion and somatic mutation.
          accession NCBI:9011618
          #molecule_type mRNA
          #residues 1-115 #label SHL
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
FEATURES
FEATURE 1-30
          region framework 1\
          domain immunoglobulin homology #label 100\
          region complementarity-determining 1\
          region framework 2\
          region complementarity-determining 2\
          region framework 3\
          region complementarity-determining 3\
          length 115 checknum 6615
SUMMARY
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pct. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
|||||
RESULT 42
ENTRY PLO237      type fragment
TITLE Ig heavy chain V region (anti-DNA, 1A11YH) - mouse (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 16-Sep-1992 sequence_revision 16-Sep-1992 text_change
ACCESSION PLO237
REFERENCE Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plautsky,
          J. Exp. Med. (1990) 171:265-297
          Anti-DNA antibodies from autoimmune mice arise by clonal
          expansion and somatic mutation.
          accession NCBI:9011618
          #molecule_type mRNA
          #residues 1-117 #label SHL
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
FEATURES
FEATURE 1-30
          region framework 1\
          domain immunoglobulin homology #label 100\
          region complementarity-determining 1\
          region framework 2\
          region complementarity-determining 2\
          region framework 3\
          region complementarity-determining 3\
          length 117 checknum 6657
SUMMARY
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pct. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
|||||
```

```
11-35      #region complementarity-determining 1\
16-49      #region framework 1\
50-66      #region complementarity-determining 2\
67-98      #region framework 2\
110-117    #region complementarity-determining 3\
SUMMARY    #length 117 checknum 6657
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pct. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
|||||
RESULT 44
ENTRY PLO236      type fragment
TITLE Ig heavy chain V region (anti-DNA, 1A11YH) - mouse (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 16-Aug-1996
ACCESSION PLO236
REFERENCE Weissenhorn, W.; Blattmuller, G.; Weiss, E.M.; Fischer, E.P.
          submitted to the EMBL Data Library, March 1992
          Structural characterization of CD4 mAb.
          accession EMBL:519566
          #molecule_type mRNA
          #residues 1-117 #label WEI
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
FEATURES
FEATURE 1-30
          region framework 1\
          domain immunoglobulin homology #label 100\
          region complementarity-determining 1\
          region framework 2\
          region complementarity-determining 2\
          region framework 3\
          region complementarity-determining 3\
          length 117 checknum 6289
SUMMARY
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pct. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
|||||
RESULT 45
ENTRY PLO234      type fragment
TITLE Ig heavy chain V region (anti-DNA, 3B9VH) - mouse (fragment)
```

```
title Anti-DNA antibodies from autoimmune mice arise by clonal
expansion and somatic mutation.
accession NCBI:9011618
#molecule_type mRNA
#residues 1-117 #label SHL
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
FEATURES
FEATURE 1-30
          region framework 1\
          domain immunoglobulin homology #label 100\
          region complementarity-determining 1\
          region framework 2\
          region complementarity-determining 2\
          region framework 3\
          region complementarity-determining 3\
          length 117 checknum 6907
SUMMARY
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pct. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
|||||
RESULT 43
ENTRY PLO235      type fragment
TITLE Ig heavy chain V region (anti-DNA, 2P2VH and 4B9VH) - mouse
ORGANISM Mus musculus (common name house mouse)
DATE 16-Sep-1992 sequence_revision 16-Sep-1992 text_change
ACCESSION PLO235
REFERENCE Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plautsky,
          J. Exp. Med. (1990) 171:265-297
          Anti-DNA antibodies from autoimmune mice arise by clonal
          expansion and somatic mutation.
          accession NCBI:9011618
          #molecule_type mRNA
          #residues 1-117 #label SHL
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
FEATURES
FEATURE 1-30
          region framework 1\
          domain immunoglobulin homology #label 100\
          region complementarity-determining 1\
          region framework 2\
          region complementarity-determining 2\
          region framework 3\
          region complementarity-determining 3\
          length 117 checknum 6907
```

```
ORGANISM Mus musculus (common name house mouse)
DATE 16-Sep-1992 sequence_revision 16-Sep-1992 text_change
ACCESSION PLO234
REFERENCE Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plautsky,
          J. Exp. Med. (1990) 171:265-297
          Anti-DNA antibodies from autoimmune mice arise by clonal
          expansion and somatic mutation.
          accession NCBI:9011618
          #molecule_type mRNA
          #residues 1-117 #label SHL
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
FEATURES
FEATURE 1-30
          region framework 1\
          domain immunoglobulin homology #label 100\
          region complementarity-determining 1\
          region framework 2\
          region complementarity-determining 2\
          region framework 3\
          region complementarity-determining 3\
          length 117 checknum 7994
SUMMARY
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pct. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
|||||
RESULT 46
ENTRY PLO231      type fragment
TITLE Ig heavy chain V region (anti-DNA, 2B9VH) - mouse (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 16-Sep-1992 sequence_revision 16-Sep-1992 text_change
ACCESSION PLO231
REFERENCE Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plautsky,
          J. Exp. Med. (1990) 171:265-297
          Anti-DNA antibodies from autoimmune mice arise by clonal
          expansion and somatic mutation.
          accession NCBI:9011618
```















371 3 1745 1 V151 CAELI HYPOTHETICAL PROTEIN P 1.0e+03  
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 398 3 1755 1 V151 CAELI HYPOTHETICAL 15.4 KD 1.0e+03  
 399 3 1755 1 V151 CAELI HYPOTHETICAL 15.4 KD 1.0e+03  
 400 3 1755 1 V151 CAELI HYPOTHETICAL 15.4 KD 1.0e+03

## ALIGNMENTS

RESULT 1  
 ID HV12 MOUSE STANDARD: PRT: 117 AA.  
 AC P01756: 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)  
 DE 10 HEAVY CHAIN V REGION (J558).  
 DE MIS MUSCULUS (MOUSE).  
 OS MUSCULUS (MOUSE).  
 OC EUTHERIA, RODENTIA.  
 RN [1]  
 RP SEQUENCE: 90078170.  
 RA SCHILLING J., CLAYINGER B., DAVID J.M., HOOD L.  
 RL NATURE 283:35-40(1980).  
 CC -1- THE SEQUENCES OF 10 HYPERIDOMA PROTEINS THAT ALSO BIND DEXTRAN  
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN

QY 34 GASTRISCASOYT 47

RESULT 3  
 ID HV12 MOUSE STANDARD: PRT: 120 AA.  
 AC P01747: 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)  
 DE 10 HEAVY CHAIN V REGION (J558).  
 DE MIS MUSCULUS (MOUSE).  
 OS MUSCULUS (MOUSE).  
 OC EUTHERIA, RODENTIA.  
 RN [1]  
 RP SEQUENCE: 90078170.  
 RA SCHILLING J., CLAYINGER B., DAVID J.M., HOOD L.  
 RL NATURE 283:35-40(1980).  
 CC -1- THE SEQUENCES OF 10 HYPERIDOMA PROTEINS THAT ALSO BIND DEXTRAN  
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN

RA SING J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,  
 CAPRA J.D., GILBERT W., GILBERT W., GILBERT W., GILBERT W.,  
 EMBL: J00493: G1510077.  
 DR PIR: A02028: HW567.  
 DR HSP: P01789: 6FAB.  
 RW HMOGLOBULIN V REGION: ANTIBODY ANTIBODY, HYPERIDOMA, SIGNAL.  
 FT CHAIN 20 140  
 FT NON\_TER 140 140  
 FT SEQUENCE 140 AA: 15514 MW: 0700058 CRC32:  
 SQ  
 Query Match 9 2% Score 14: DB 1: Length 140.  
 Best Local Similarity 100.0%: Pred. No. 4,59e-17.  
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 DB 104 STREDSAYVCA 117  
 QY 104 STREDSAYVCA 117  
 RESULT 4  
 ID HV12 MOUSE STANDARD: PRT: 140 AA.  
 AC P01746: 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)  
 DE 10 HEAVY CHAIN V REGION (J558).  
 DE MIS MUSCULUS (MOUSE).  
 OS MUSCULUS (MOUSE).  
 OC EUTHERIA, RODENTIA.  
 RN [1]  
 RP SEQUENCE: 90078170.  
 RA SCHILLING J., CLAYINGER B., DAVID J.M., HOOD L.  
 RL NATURE 283:35-40(1980).  
 CC -1- THE SEQUENCES OF 10 HYPERIDOMA PROTEINS THAT ALSO BIND DEXTRAN  
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN

CC THE D AND J SEGMENTS.  
 CC -1- THIS PROTEIN BINDS DEXTRAN.  
 DR PIR: A02028: HW567.  
 DR HSP: P01789: 6FAB.  
 RW HMOGLOBULIN V REGION: ANTIBODY ANTIBODY, HYPERIDOMA, SIGNAL.  
 FT CHAIN 20 140  
 FT NON\_TER 140 140  
 FT SEQUENCE 140 AA: 15514 MW: 0700058 CRC32:  
 SQ  
 Query Match 9 2% Score 14: DB 1: Length 140.  
 Best Local Similarity 100.0%: Pred. No. 4,59e-17.  
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 DB 104 STREDSAYVCA 117  
 QY 104 STREDSAYVCA 117  
 RESULT 5  
 ID HV12 MOUSE STANDARD: PRT: 144 AA.  
 AC P01819: 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)  
 DE 10 HEAVY CHAIN V REGION (J558).  
 DE MIS MUSCULUS (MOUSE).  
 OS MUSCULUS (MOUSE).  
 OC EUTHERIA, RODENTIA.  
 RN [1]  
 RP SEQUENCE: 90078170.  
 RA SCHILLING J., CLAYINGER B., DAVID J.M., HOOD L.  
 RL NATURE 283:35-40(1980).  
 CC -1- THE SEQUENCES OF 10 HYPERIDOMA PROTEINS THAT ALSO BIND DEXTRAN  
 CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN



FT CHAIN 20 117 10 HEAVY CHAIN V REGION (10A).  
 SEQUENCE 117 AA: 12972 MW: 9410002 CRC32:  
 Query Match: 7.2% Score 11: DB 1: Length 117;  
 Best Local Similarity 100.0% Pred. No. 1,546-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 SLSITSESNVY 113  
 103 SLSITSESNVY 113

RESULT 11 STANDARD: PRT: 117 AA.  
 AC P06328:  
 DT 01-JAN-1986 (REL. 06, CREATED)  
 DT 21-JUL-1986 (REL. 06, LAST SEQUENCE UPDATE)  
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH58 B4).  
 OS MUS MUSCULUS (MOUSE).  
 CC EPIHATROTA; METALON; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
 OC EPIHATROTA; RODENTIA.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 85099340.  
 RA BOTHEWELL A.L.M., PARKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,  
 DR EMBL: 401312811(1985).  
 DR PIR: A02035; M08584.  
 DR HSP: P01810; 12HL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 20 117 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON-TER 117 117  
 SEQUENCE 117 AA: 12834 MW: 8569285 CRC32:  
 Query Match: 7.2% Score 11: DB 1: Length 117;  
 Best Local Similarity 100.0% Pred. No. 1,546-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 SLSITSESNVY 113  
 103 SLSITSESNVY 113

OS MUS MUSCULUS (MOUSE).  
 OC EPIHATROTA; METALON; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
 CC EPIHATROTA; RODENTIA.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 81234548.  
 RA BOTHEWELL A.L.M., PARKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,  
 DR EMBL: 401312811(1985).  
 DR PIR: A02035; M08584.  
 DR HSP: P01810; 12HL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 20 117 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON-TER 117 117  
 SEQUENCE 117 AA: 12921 MW: 8569000 CRC32:  
 Query Match: 7.2% Score 11: DB 1: Length 117;  
 Best Local Similarity 100.0% Pred. No. 1,546-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 SLSITSESNVY 113  
 103 SLSITSESNVY 113

RESULT 11 STANDARD: PRT: 121 AA.  
 AC P06328:  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH58 B4).  
 OS MUS MUSCULUS (MOUSE).  
 CC EPIHATROTA; METALON; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
 OC EPIHATROTA; RODENTIA.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 81051741.  
 RA ZAKUT R., COHEN J., GIVOL D.,  
 DR EMBL: 401312811(1985).  
 DR PIR: A02035; M08584.  
 DR HSP: P01810; 12HL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 20 117 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON-TER 117 117  
 SEQUENCE 117 AA: 12921 MW: 8569000 CRC32:  
 Query Match: 7.2% Score 11: DB 1: Length 117;  
 Best Local Similarity 100.0% Pred. No. 1,546-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 SLSITSESNVY 113  
 103 SLSITSESNVY 113

RESULT 12 STANDARD: PRT: 117 AA.  
 AC P01748:  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH58 B4).  
 OS MUS MUSCULUS (MOUSE).  
 CC EPIHATROTA; METALON; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
 OC EPIHATROTA; RODENTIA.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 81234548.  
 RA BOTHEWELL A.L.M., PARKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,  
 DR EMBL: 401312811(1985).  
 DR PIR: A02035; M08584.  
 DR HSP: P01810; 12HL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 20 117 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON-TER 117 117  
 SEQUENCE 117 AA: 13016 MW: 8569285 CRC32:  
 Query Match: 7.2% Score 11: DB 1: Length 117;  
 Best Local Similarity 100.0% Pred. No. 1,546-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 60 P01748: 70  
 60 P01748: 70

RP REVISIONS.  
 RA ZAKUT R., COHEN J., GIVOL D.,  
 DR EMBL: 401312811(1985).  
 DR PIR: A02035; M08584.  
 DR HSP: P01810; 12HL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 20 117 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON-TER 117 117  
 SEQUENCE 121 AA: 13135 MW: 2868000 CRC32:  
 Query Match: 7.2% Score 11: DB 1: Length 121;  
 Best Local Similarity 100.0% Pred. No. 1,546-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 70 LNDITSESNVY 80  
 80 LNDITSESNVY 99

RESULT 15 STANDARD: PRT: 137 AA.  
 AC P01754:  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH58 B4).  
 OS MUS MUSCULUS (MOUSE).  
 CC EPIHATROTA; METALON; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.  
 OC EPIHATROTA; RODENTIA.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 81234548.  
 RA BOTHEWELL A.L.M., PARKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,  
 DR EMBL: 401312811(1985).  
 DR PIR: A02035; M08584.  
 DR HSP: P01810; 12HL.  
 KW IMMUNOGLOBULIN V REGION; SIGNAL.  
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 20 117 10 HEAVY CHAIN V REGION (VH58 B4).  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON-TER 117 117  
 SEQUENCE 137 AA: 13222 MW: 2868000 CRC32:  
 Query Match: 7.2% Score 11: DB 1: Length 137;  
 Best Local Similarity 100.0% Pred. No. 1,546-09;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 60 P01754: 70  
 60 P01754: 70







PT	NON_TER	130	130
SQ	SEQUENCE	130 AA;	14320 MW; BFB718FB CRC32;

DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)

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PT NON_TER 130 130
SQ SEQUENCE 130 AA; 14320 MM; BFB718FB CRC32;
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DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)

DE T-CELL RECEPTOR BETA CHAIN PRECURSOR V REGION (Y735).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 DE EUTHERIA: PRIMATES.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 8414269.  
 RA YANAGI, Y., YOSHIDA, Y., LECGERT, K., CLARK, S.P., ALEXANDER, I.,  
 DR PIR: A020001.FRM00Y.  
 DR HSP: P01607.12NM.  
 RM T-CELL RECEPTOR: SIGNAL.  
 FT CHAIN 1 115  
 FT NON-TER 135 115  
 SQ SEQUENCE 135 AA: 15097 MW: 4080855 CRC32:  
 Query Match 5.24: Score 8: DB 1: Length 135:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 105 DASYFCA 112  
 Oy 109 DASYFCA 116

RESULT 33  
 ID TPA2.JOMAN STANDARD: PRT: 139 AA.  
 AC P04437.  
 DT 21-JUL-1986 (REL. 05, CREATED)  
 DT 21-JUL-1986 (REL. 05, LAST SEQUENCE UPDATE)  
 DE T-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-117).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 DE EUTHERIA: PRIMATES.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 8527670.  
 RA BERNICH, H.H., JOHANSSON, S.G.O., STRONINGER, J.L.,  
 DR PIR: A02028.12NM.  
 DR HSP: P01607.12NM.  
 RM T-CELL RECEPTOR: GLYCOPROTEIN: SIGNAL.  
 FT CHAIN 28 139  
 FT NON-TER 27 139  
 SQ SEQUENCE 139 AA: 15097 MW: 4080855 CRC32:  
 Query Match 5.24: Score 8: DB 1: Length 135:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 105 DASYFCA 112  
 Oy 109 DASYFCA 116

FT NON-TER 143 143  
 SQ SEQUENCE 143 AA: 16051 MW: 6060581 CRC32:  
 Query Match 5.24: Score 8: DB 1: Length 143:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 36 SCLASCT 43  
 Oy 40 SCLASCT 47

RESULT 35  
 ID TPA2.JOMAN STANDARD: PRT: 111 AA.  
 AC P01804.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE T-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-117).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 DE EUTHERIA: PRIMATES.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 8101317.  
 RA BERNICH, H.H., JOHANSSON, S.G.O., STRONINGER, J.L.,  
 DR PIR: A020001.FRM00Y.  
 DR HSP: P01607.12NM.  
 RM T-CELL RECEPTOR: SIGNAL.  
 FT CHAIN 1 111  
 FT NON-TER 111 111  
 SQ SEQUENCE 111 AA: 12304 MW: 13340848 CRC32:  
 Query Match 4.54: Score 7: DB 1: Length 111:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 99 DASYFCA 105  
 Oy 125 DASYFCA 131

RESULT 36  
 ID TPA2.JOMAN STANDARD: PRT: 115 AA.  
 AC P01765.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

FT DOMAIN 28 120  
 FT DOMAIN 126 119  
 FT DOMAIN 126 119  
 FT CARBOXY 93 93  
 FT DISORDERED 49 116  
 FT DISORDERED 139 119  
 SQ SEQUENCE 139 AA: 15644 MW: 8263141 CRC32:  
 Query Match 5.24: Score 8: DB 1: Length 139:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 110 DASYFCA 117  
 Oy 109 DASYFCA 116

RESULT 34  
 ID TPA2.JOMAN STANDARD: PRT: 143 AA.  
 AC P04437.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE T-CELL RECEPTOR ALPHA CHAIN PRECURSOR V-I REGION (HND) (FRAGMENTS).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 DE EUTHERIA: PRIMATES.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 8306314.  
 RA BELL, L.O., COULD, H.J.,  
 DR PIR: A02028.12NM.  
 DR HSP: P01607.12NM.  
 RM T-CELL RECEPTOR: SIGNAL.  
 FT CHAIN 1 143  
 FT NON-TER 143 143  
 SQ SEQUENCE 143 AA: 15097 MW: 4080855 CRC32:  
 Query Match 5.24: Score 8: DB 1: Length 143:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 105 DASYFCA 112  
 Oy 109 DASYFCA 116

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE T-CELL RECEPTOR ALPHA CHAIN PRECURSOR V-I REGION (HND).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 DE EUTHERIA: PRIMATES.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 7800558.  
 RA WANG, A.-C., YANG, I.-Y., FUDENBERG, H.H.,  
 DR PIR: A02028.12NM.  
 DR HSP: P01607.12NM.  
 RM T-CELL RECEPTOR: SIGNAL.  
 FT CHAIN 1 143  
 FT NON-TER 143 143  
 SQ SEQUENCE 143 AA: 15097 MW: 4080855 CRC32:  
 Query Match 5.24: Score 8: DB 1: Length 143:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 105 DASYFCA 112  
 Oy 125 DASYFCA 131

RESULT 37  
 ID TPA2.JOMAN STANDARD: PRT: 116 AA.  
 AC P01983.  
 DT 21-JUL-1986 (REL. 02, CREATED)  
 DT 21-JUL-1986 (REL. 02, LAST SEQUENCE UPDATE)  
 DE T-CELL RECEPTOR ALPHA CHAIN PRECURSOR V-I REGION (HND) (FRAGMENTS).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 DE EUTHERIA: PRIMATES.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 8516276.  
 RA LITMAN, G.W., BERGER, L., KIRBY, K., LITMAN, R., HINDS, K.,  
 DR PIR: A02028.12NM.  
 DR HSP: P01607.12NM.  
 RM T-CELL RECEPTOR: SIGNAL.  
 FT CHAIN 1 116  
 FT NON-TER 116 116  
 SQ SEQUENCE 116 AA: 12304 MW: 13340848 CRC32:  
 Query Match 4.54: Score 7: DB 1: Length 116:  
 Best Local Similarity 100.0%: Pred. No. 7.61e-03:  
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 Db 99 DASYFCA 105  
 Oy 125 DASYFCA 131





DB 49 LSLITTO 55  
QY 10 LSLITTO 16

RESULT 48  
ID YCBA\_METZA STANDARD: PRT: 254 AA.  
AC P81318: 1998 (REL. 16, CREATED)  
DT 15-JUL-1998 (REL. 16, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 16, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL PROTEIN M1282.1.  
CM M1282.1: LOCUS JANUSCHIT  
CC ARCHAEABACTERIA: EUBACTERIA: METHANOCOCCALES: METHANOCOCCACEAE.  
RN (1)  
RP SEQUENCE FROM N.A. 2661 / ATCC 43067.  
RC STRAIN: M1282.1, DSM 2661 / ATCC 43067.  
RA BLITZ C.J., WHITE O., OLSEN G.J., EROU L., FLEISCHMAN R.D.,  
RA SUTTON G.C., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., COOKE J.D.,  
RA KRIEGLER A.R., DOUGHERTY B.A., TONG J.P., ADAMS M.D., REICH C.I.,  
RA SCOTT J.N., GEORGE S.M., NEIDMAN J.S., FISHMAN S.L., GUTENBERG  
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SALOW P.M., HANNA M.C.,  
RA COTTON M.D., ROBERTS R.M., ERNST M.A., KATZ B.P., BOROSOVITZ M.,  
RA KLEIN H.J., FRASER C.M., SMITH R.O., MOSE C.R., YAMTER J.C.,  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO M. JANUSCHIT M10902.  
DR EMBL: 057569: G2863589.  
DN TIGR: M1282.1.  
RN ARCHAEABACTERIA: EUBACTERIA: TRANSDOMINANT.  
FT TRANSDOMINANT 33 53 POTENTIAL.  
FT TRANSDOMINANT 70 90 POTENTIAL.  
FT TRANSDOMINANT 92 112 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
SQ SEQUENCE 254 AA: 23965 MW: 05320000 CRC13:  
Query Match 4.6% Score 7: DB 1: Length 254;  
Query Local Similarity 100.0% Pred. No. 6.73e-01;  
Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0.

DB 78 VLFILS 84  
QY 6 VLFILS 12

RESULT 49

DB 143 LSLITTO 149  
QY 10 LSLITTO 16

RESULT 50  
ID DINO MOOSE STANDARD: PRT: 273 AA.  
AC P81318: 1998 (REL. 16, CREATED)  
DT 01-NOV-1997 (REL. 16, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 16, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL PROTEIN M1282.1.  
CM M1282.1: LOCUS JANUSCHIT  
CC ARCHAEABACTERIA: EUBACTERIA: METHANOCOCCALES: METHANOCOCCACEAE.  
RN (1)  
RP SEQUENCE FROM N.A. 2661 / ATCC 43067.  
RC STRAIN: M1282.1, DSM 2661 / ATCC 43067.  
RA BLITZ C.J., WHITE O., OLSEN G.J., EROU L., FLEISCHMAN R.D.,  
RA SUTTON G.C., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., COOKE J.D.,  
RA KRIEGLER A.R., DOUGHERTY B.A., TONG J.P., ADAMS M.D., REICH C.I.,  
RA SCOTT J.N., GEORGE S.M., NEIDMAN J.S., FISHMAN S.L., GUTENBERG  
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SALOW P.M., HANNA M.C.,  
RA COTTON M.D., ROBERTS R.M., ERNST M.A., KATZ B.P., BOROSOVITZ M.,  
RA KLEIN H.J., FRASER C.M., SMITH R.O., MOSE C.R., YAMTER J.C.,  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO M. JANUSCHIT M10902.  
DR EMBL: 057569: G2863589.  
DN TIGR: M1282.1.  
RN ARCHAEABACTERIA: EUBACTERIA: TRANSDOMINANT.  
FT TRANSDOMINANT 33 53 POTENTIAL.  
FT TRANSDOMINANT 70 90 POTENTIAL.  
FT TRANSDOMINANT 92 112 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
SQ SEQUENCE 254 AA: 23965 MW: 05320000 CRC13:  
Query Match 4.6% Score 7: DB 1: Length 254;  
Query Local Similarity 100.0% Pred. No. 6.73e-01;  
Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0.

DB 143 LSLITTO 149  
QY 10 LSLITTO 16

RESULT 50  
ID DINO MOOSE STANDARD: PRT: 273 AA.  
AC P81318: 1998 (REL. 16, CREATED)  
DT 01-NOV-1997 (REL. 16, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 16, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL PROTEIN M1282.1.  
CM M1282.1: LOCUS JANUSCHIT  
CC ARCHAEABACTERIA: EUBACTERIA: METHANOCOCCALES: METHANOCOCCACEAE.  
RN (1)  
RP SEQUENCE FROM N.A. 2661 / ATCC 43067.  
RC STRAIN: M1282.1, DSM 2661 / ATCC 43067.  
RA BLITZ C.J., WHITE O., OLSEN G.J., EROU L., FLEISCHMAN R.D.,  
RA SUTTON G.C., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., COOKE J.D.,  
RA KRIEGLER A.R., DOUGHERTY B.A., TONG J.P., ADAMS M.D., REICH C.I.,  
RA SCOTT J.N., GEORGE S.M., NEIDMAN J.S., FISHMAN S.L., GUTENBERG  
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SALOW P.M., HANNA M.C.,  
RA COTTON M.D., ROBERTS R.M., ERNST M.A., KATZ B.P., BOROSOVITZ M.,  
RA KLEIN H.J., FRASER C.M., SMITH R.O., MOSE C.R., YAMTER J.C.,  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO M. JANUSCHIT M10902.  
DR EMBL: 057569: G2863589.  
DN TIGR: M1282.1.  
RN ARCHAEABACTERIA: EUBACTERIA: TRANSDOMINANT.  
FT TRANSDOMINANT 33 53 POTENTIAL.  
FT TRANSDOMINANT 70 90 POTENTIAL.  
FT TRANSDOMINANT 92 112 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
SQ SEQUENCE 254 AA: 23965 MW: 05320000 CRC13:  
Query Match 4.6% Score 7: DB 1: Length 254;  
Query Local Similarity 100.0% Pred. No. 6.73e-01;  
Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0.

DB 143 LSLITTO 149  
QY 10 LSLITTO 16

RESULT 50  
ID DINO MOOSE STANDARD: PRT: 273 AA.  
AC P81318: 1998 (REL. 16, CREATED)  
DT 01-NOV-1997 (REL. 16, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 16, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL PROTEIN M1282.1.  
CM M1282.1: LOCUS JANUSCHIT  
CC ARCHAEABACTERIA: EUBACTERIA: METHANOCOCCALES: METHANOCOCCACEAE.  
RN (1)  
RP SEQUENCE FROM N.A. 2661 / ATCC 43067.  
RC STRAIN: M1282.1, DSM 2661 / ATCC 43067.  
RA BLITZ C.J., WHITE O., OLSEN G.J., EROU L., FLEISCHMAN R.D.,  
RA SUTTON G.C., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., COOKE J.D.,  
RA KRIEGLER A.R., DOUGHERTY B.A., TONG J.P., ADAMS M.D., REICH C.I.,  
RA SCOTT J.N., GEORGE S.M., NEIDMAN J.S., FISHMAN S.L., GUTENBERG  
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SALOW P.M., HANNA M.C.,  
RA COTTON M.D., ROBERTS R.M., ERNST M.A., KATZ B.P., BOROSOVITZ M.,  
RA KLEIN H.J., FRASER C.M., SMITH R.O., MOSE C.R., YAMTER J.C.,  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO M. JANUSCHIT M10902.  
DR EMBL: 057569: G2863589.  
DN TIGR: M1282.1.  
RN ARCHAEABACTERIA: EUBACTERIA: TRANSDOMINANT.  
FT TRANSDOMINANT 33 53 POTENTIAL.  
FT TRANSDOMINANT 70 90 POTENTIAL.  
FT TRANSDOMINANT 92 112 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
SQ SEQUENCE 254 AA: 23965 MW: 05320000 CRC13:  
Query Match 4.6% Score 7: DB 1: Length 254;  
Query Local Similarity 100.0% Pred. No. 6.73e-01;  
Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0.

DB 143 LSLITTO 149  
QY 10 LSLITTO 16

RESULT 50  
ID DINO MOOSE STANDARD: PRT: 273 AA.  
AC P81318: 1998 (REL. 16, CREATED)  
DT 01-NOV-1997 (REL. 16, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 16, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL PROTEIN M1282.1.  
CM M1282.1: LOCUS JANUSCHIT  
CC ARCHAEABACTERIA: EUBACTERIA: METHANOCOCCALES: METHANOCOCCACEAE.  
RN (1)  
RP SEQUENCE FROM N.A. 2661 / ATCC 43067.  
RC STRAIN: M1282.1, DSM 2661 / ATCC 43067.  
RA BLITZ C.J., WHITE O., OLSEN G.J., EROU L., FLEISCHMAN R.D.,  
RA SUTTON G.C., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., COOKE J.D.,  
RA KRIEGLER A.R., DOUGHERTY B.A., TONG J.P., ADAMS M.D., REICH C.I.,  
RA SCOTT J.N., GEORGE S.M., NEIDMAN J.S., FISHMAN S.L., GUTENBERG  
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SALOW P.M., HANNA M.C.,  
RA COTTON M.D., ROBERTS R.M., ERNST M.A., KATZ B.P., BOROSOVITZ M.,  
RA KLEIN H.J., FRASER C.M., SMITH R.O., MOSE C.R., YAMTER J.C.,  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO M. JANUSCHIT M10902.  
DR EMBL: 057569: G2863589.  
DN TIGR: M1282.1.  
RN ARCHAEABACTERIA: EUBACTERIA: TRANSDOMINANT.  
FT TRANSDOMINANT 33 53 POTENTIAL.  
FT TRANSDOMINANT 70 90 POTENTIAL.  
FT TRANSDOMINANT 92 112 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
FT TRANSDOMINANT 123 123 POTENTIAL.  
SQ SEQUENCE 254 AA: 23965 MW: 05320000 CRC13:  
Query Match 4.6% Score 7: DB 1: Length 254;  
Query Local Similarity 100.0% Pred. No. 6.73e-01;  
Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0.

CC EMBL: 012961: G595518  
DR EMBL: 575951: G913783  
DR KGD: M61:103187: NCOR1  
DR KGD: M61:103187: NCOR1  
FT INITIATION  
FT MOD\_RES 1  
SO SEQUENCE 273 AA: 30828 MW: 8603955 CMC12;  
ACETYLATION

Query Match 1.64 Score 7; DB 1: Length 273;  
Best Local Similarity 100.0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 143 LISTING 149  
QY 10 LISTING 16

Search completed: Thu Apr 15 18:09:11 1999  
Job time : 53 secs.



!!SEQUENCE\_LIST 1.0  
(peptide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-4 check: 265 from: 1

FROMIG of: /home/obryen/ree455/olig/us08836455.pep  
sequence 4, application us/08836455

general information:  
applicant: chatterjee, malaya  
applicant: foon, kenneth a.  
applicant: chatterjee, sunil k. . .

TO: swp:\* Sequences: 254,782 Total-length: 82,009,484 April 18, 1999 19:50

Database Release Information:

2 db's { SWISS-PROT, Release 36.0, Released on 18Aug1998, Formatted on 18Aug1998  
SPRMBL, Release 8.0, Released on 21Nov1998, Formatted on 15Dec1998  
Word-size: 5 Words: 52398 Diagonals: 10,097 Total Diagonals: 120,736,348  
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 9.48

Sequence . . . . . SIRD Diag Score Width Documentation . .

SM:HV06_MOUSE	+	0	66	1	P01750	mus musculus (mouse).	1g heavy
SM:HV02_MOUSE	+	0	64	1	P01746	mus musculus (mouse).	1g heavy
SM:HV14_MOUSE	+	0	61	1	P01758	mus musculus (mouse).	1g heavy
SM:HV03_MOUSE	+	-20	58	1	P01747	mus musculus (mouse).	1g heavy
SM:HV09_MOUSE	+	0	56	1	P01753	mus musculus (mouse).	1g heavy
SM:HV05_MOUSE	+	0	56	1	P01749	mus musculus (mouse).	1g heavy
SM:HV52_MOUSE	+	0	56	1	P06327	mus musculus (mouse).	1g heavy
SM:HV49_MOUSE	+	0	55	1	P06328	mus musculus (mouse).	1g heavy
SM:HV07_MOUSE	+	0	54	1	P01751	mus musculus (mouse).	1g heavy
SM:HV04_MOUSE	+	0	52	1	P01748	mus musculus (mouse).	1g heavy
SM:HV13_MOUSE	+	-19	51	2	P01757	mus musculus (mouse).	1g heavy
SM:HV12_MOUSE	+	-19	51	2	P01756	mus musculus (mouse).	1g heavy
SM:HV51_MOUSE	+	0	50	1	P01755	mus musculus (mouse).	1g heavy
SM:HV51_MOUSE	+	-19	47	1	P06330	mus musculus (mouse).	1g heavy
SM:HV10_MOUSE	+	0	46	1	P01754	mus musculus (mouse).	1g heavy
SM:HV15_MOUSE	+	0	38	2	P01759	mus musculus (mouse).	1g heavy
SM:HV01_MOUSE	+	-19	36	1	P01745	mus musculus (mouse).	1g heavy
SM:HV00_MOUSE	+	-19	34	1	P01741	mus musculus (mouse).	1g heavy
SM:HV48_MOUSE	+	0	33	2	P03980	mus musculus (mouse).	1g heavy
SM:HV1G_HUMAN	+	0	30	1	P23083	homo sapiens (human).	1g heavy
SM:HV1B_HUMAN	+	0	25	1	P01743	homo sapiens (human).	1g heavy
SM:HV50_MOUSE	+	-19	25	1	P06329	mus musculus (mouse).	1g heavy
SM:HV1C_HUMAN	+	-4	18	1	P01744	homo sapiens (human).	1g heavy
SM:HV1A_HUMAN	+	-19	18	2	P01742	homo sapiens (human).	1g heavy
SP.HDM:015224	+	-110	18	1	O15224	homo sapiens (human).	cdt-3-igm
SM:HV43_MOUSE	+	-1	14	1	P01819	mus musculus (mouse).	1g heavy
SM:HV16_MOUSE	+	-1	13	1	P01783	mus musculus (mouse).	1g heavy
SM:HV02_XENLA	+	-12	13	1	P20957	xenopus laevis (african clawed	
SM:HV37_MOUSE	+	-19	12	1	P01807	mus musculus (mouse).	1g heavy
SM:HV42_MOUSE	+	-19	12	2	P01812	mus musculus (mouse).	1g heavy
SM:HV40_MOUSE	+	-19	12	1	P01810	mus musculus (mouse).	1g heavy
SM:HV3K_HUMAN	+	-11	12	1	P01772	homo sapiens (human).	1g heavy
SM:HV3G_HUMAN	+	-15	11	1	P01768	homo sapiens (human).	1g heavy
SM:HV38_MOUSE	+	-19	11	1	P01808	mus musculus (mouse).	1g heavy
SM:HV2C_RABIT	+	-1	11	1	P01829	oryctolagus cuniculus (rabbit)	
SM:HV2C_HUMAN	+	-18	11	1	P01816	homo sapiens (human).	1g heavy
SM:HV1E_HUMAN	+	-15	11	1	P01761	homo sapiens (human).	1g heavy
SM:HV1D_HUMAN	+	-15	11	1	P01760	homo sapiens (human).	1g heavy
SM:HV03_CAICR	+	0	11	1	P03962	calman crocodilus (spectacled	
SM:HV01_RAT	+	5	11	1	P01805	rattus norvegicus (rat).	1g he
SM:HV01_CANFA	+	-23	11	1	P01784	canis familiaris (dog).	1g he
SP.HDM:P78465	+	-125	11	1	P78465	homo sapiens (human).	follicul
SM:HV41_MOUSE	+	-19	11	2	P01811	mus musculus (mouse).	1g heavy
SM:HV3J_HUMAN	+	-16	11	1	P01771	homo sapiens (human).	1g heavy
SM:HV3I_HUMAN	+	-18	10	1	P01770	homo sapiens (human).	1g heavy
SM:HV3B_HUMAN	+	-23	10	1	P01763	homo sapiens (human).	1g heavy
SM:HV2I_HUMAN	+	9	10	1	P06331	homo sapiens (human).	1g heavy
SM:HV2D_HUMAN	+	-12	10	1	P01817	homo sapiens (human).	1g heavy
SM:HV1C_HUMAN	+	6	10	1	P01744	homo sapiens (human).	1g heavy
SM:HV3U_HUMAN	+	-17	10	1	P01782	homo sapiens (human).	1g heavy

at least 5 aa long

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966 5 3.3 1011 14 081754 POLYPROTEIN. 1.66e+03
969 5 3.3 1011 14 036608 POLYPROTEIN. 1.66e+03
970 5 3.3 1011 14 036610 POLYPROTEIN. 1.66e+03
971 5 3.3 1011 14 036609 POLYPROTEIN. 1.66e+03
972 5 3.3 1021 14 081850 GENES FOR COX2, ENVELO 1.66e+03
973 5 3.3 1021 14 081850 POLYPROTEIN. 1.66e+03
974 5 3.3 1022 14 081858 POLYPROTEIN. 1.66e+03
975 5 3.3 1022 14 081858 POLYPROTEIN. 1.66e+03
976 5 3.3 1022 14 081858 POLYPROTEIN. 1.66e+03
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985 5 3.3 1022 14 081858 POLYPROTEIN. 1.66e+03
986 5 3.3 1022 14 081858 POLYPROTEIN. 1.66e+03
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## ALIGNMENTS

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RESULT 1
ID 009199 PRELIMINARY: PRT: 118 AA.
AC 009199:
DT 01-JUN-1997 (TREMBL, 04, CREATED)
DT 01-JUN-1997 (TREMBL, 04, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBL, 06, LAST ANNOTATION UPDATE)
DE IGM HEAVY CHAIN (FRAGMENT).
OS UNKNOWN.
OC UNCLASSIFIED.
RN [1]
RP SEQUENCE FROM N.A.
RA PAYELLE-BROCARD B.;
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

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OS MUS MUSCULUS (MOUSE).
OC EUTHERIA, RODENTIA.
RA KINOMOTO H., YOSHIMIZU H., TANAKA K.;
DR EMBL: 582857, G153586;
DR PDB: PFO0047, 19.
FT NON_TER 1
SQ SEQUENCE 120 AA: 13147 MW: 325408 CRC32.
Query Match
Best Local Similarity 100.0%; Pred. No. 1,10e-17; Length 120;
Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 14 GASTRASCASGTT 27
QY 34 GASTRASCASGTT 47

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DR EMBL: 044924; G1763745;
DR PDB: PFO0047, 19.
FT NON_TER 1
SQ SEQUENCE 118 AA: 13117 MW: 0983865 CRC32.
Query Match
Best Local Similarity 100.0%; Pred. No. 2,08e-20; Length 118;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 84 SEITSENAYVCAR 98
QY 103 SEITSENAYVCAR 117

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Mon Apr 19 13:24:01 1999

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RESULT 3
ID 009746 PRELIMINARY: PRT: 120 AA.
AC 009746:
DT 01-MAY-1997 (TREMBL, 03, CREATED)
DT 01-MAY-1997 (TREMBL, 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBL, 06, LAST ANNOTATION UPDATE)
DE IGM HEAVY CHAIN (FRAGMENT).
OS UNKNOWN.
OC UNCLASSIFIED.
RN [1]
RP SEQUENCE FROM N.A.
RA PAYELLE-BROCARD B.;
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 044925; G1763747;
DR PDB: PFO0047, 19.
FT NON_TER 1
SQ SEQUENCE 118 AA: 12937 MW: PFO0047 CRC32.
Query Match
Best Local Similarity 100.0%; Pred. No. 1,10e-17; Length 118;
Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 GASTRASCASGTT 28
QY 34 GASTRASCASGTT 47

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RA BATESCH H., KOLA A., KLOS A., KOSCH T.  
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AJ225590; E2187529; -.  
KW PNASID.  
FT NON\_TER 1 1  
FT NON\_TER 121 122  
SQ SEQUENCE 121 AA: 13255 MW; A63C9DD CRC32:

Query Match 8.5%: Score 13; DB 11; Length 121;  
Best Local Similarity 100.0%; Pred. No. 5.1e-15;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 108 DINGOCTSYTSS 120  
QY 125 DINGOCTSYTSS 137

RESULT 7 PRELIMINARY: PRT: 152 AA.

ID 061550  
AC 061552  
DT 01-NOV-1996 (TREMBL:01, CREATED)  
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBL:06, LAST ANNOTATION UPDATE)  
DE ANTI-HV-1 REVERSE TRANSCRIPTASE PRECURSOR.  
DE CCA-433 PRECURSOR (FRAGMENT).  
DE MUS MUSCULUS (MOUSE).  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: RODENTIA.  
RN 11  
RS SEQUENCE FROM N.A.  
RC STRAIN: BALB/C.  
RA MEDLINE: 96114009.  
RL THIRION S., MONTAN R., HETZIGEN H., RAUS J., VANDEVYVER C.;  
INMODOGENETICS 43:167-168(1996).  
DR PNAS: P00047; 15.  
KW SIGNAL.

FT CHAIN 1 19 POTENTIAL.  
FT SIGNAL 20 152 ANTIEN, B-CELL RECEPTOR.  
SQ SEQUENCE 152 AA: 16517 MW; A5E9253 CRC32:

Query Match 8.5%: Score 13; DB 11; Length 152;  
Best Local Similarity 100.0%; Pred. No. 5.1e-15;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 34 GASTRINSCASCT 46  
QY 34 GASTRINSCASCT 46

RESULT 8 PRELIMINARY: PRT: 262 AA.

Query Match 7.8%: Score 12; DB 11; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.9e-12;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 104 SLTSDSNVYR 115  
QY 104 SLTSDSNVYR 115

RESULT 10 PRELIMINARY: PRT: 243 AA.

ID 051140  
AC 051142  
DT 01-JAN-1998 (TREMBL:05, CREATED)  
DT 01-JAN-1998 (TREMBL:05, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBL:07, LAST ANNOTATION UPDATE)  
DE MUS MUSCULUS (MOUSE).  
DE REGION (FRAGMENT).  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: RODENTIA.  
RN 11  
RS SEQUENCE FROM N.A.  
RC STRAIN: BALB/C.  
RA KLINER A., BARTH S., MATTHEI B., LEMKE H., ARENDZ J.W., DIEHL V.,  
HOOGENBOOM H., ENGERT A.;  
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: D00233; G2250774; -.  
KW SIGNAL.

FT NON\_TER 1 19  
FT NON\_TER 243 243  
SQ SEQUENCE 243 AA: 26225 MW; E0AD5183 CRC32:

Query Match 7.2%: Score 11; DB 11; Length 243;  
Best Local Similarity 100.0%; Pred. No. 6.97e-10;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 18 VMSCHASCT 28  
QY 37 VMSCHASCT 47

RESULT 11 PRELIMINARY: PRT: 37 AA.

ID 053114  
AC 053116  
DT 01-JUN-1998 (TREMBL:06, CREATED)  
DT 01-JUN-1998 (TREMBL:06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBL:06, LAST ANNOTATION UPDATE)  
DE E3 ANTI-14-HYDROXY-3-NITROPHENYL-PHENOLATE + PHENOLIC FORM] ACETYL  
DE MAB V-H REGION (FRAGMENT).  
DE REGION (FRAGMENT).  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: RODENTIA.  
RN 11  
RS SEQUENCE FROM N.A.  
RC STRAIN: BALB/C.  
RA KLINER A., BARTH S., MATTHEI B., LEMKE H., ARENDZ J.W., DIEHL V.,  
HOOGENBOOM H., ENGERT A.;  
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: D00233; G2250774; -.  
KW SIGNAL.

AC 051842  
DT 01-JAN-1998 (TREMBL:05, CREATED)  
DT 01-JAN-1998 (TREMBL:05, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBL:07, LAST ANNOTATION UPDATE)  
DE ANTI-HV-1 REVERSE TRANSCRIPTASE SINGLE-CHAIN VARIABLE FRAGMENT.  
DE CCA-433 PRECURSOR (FRAGMENT).  
DE MUS MUSCULUS (MOUSE).  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: RODENTIA.  
RN 11  
RS SEQUENCE FROM N.A.  
RC STRAIN: BALB/C.  
RA MEDLINE: 96211469.  
RL SHAHREK F., DUAN L., SHU M., BAGASRA O., POKERANTZ R.J.;  
J. VIROL. 70:1392-1400(1996).  
DR PNAS: P00047; 15.  
KW SIGNAL.

FT CHAIN 1 19 POTENTIAL.  
FT SIGNAL 20 152 ANTIEN, B-CELL RECEPTOR.  
SQ SEQUENCE 152 AA: 16517 MW; A5E9253 CRC32:

Query Match 8.5%: Score 13; DB 11; Length 262;  
Best Local Similarity 100.0%; Pred. No. 5.1e-15;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 350 DINGOCTSYTSS 262  
QY 125 DINGOCTSYTSS 137

RESULT 9 PRELIMINARY: PRT: 134 AA.

ID 061552  
AC 061552  
DT 01-NOV-1996 (TREMBL:01, CREATED)  
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBL:06, LAST ANNOTATION UPDATE)  
DE ANTI-HV-1 REVERSE TRANSCRIPTASE PRECURSOR.  
DE CCA-433 PRECURSOR (FRAGMENT).  
DE MUS MUSCULUS (MOUSE).  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: RODENTIA.  
RN 11  
RS SEQUENCE FROM N.A.  
RC STRAIN: BALB/C.  
RA MEDLINE: 96114009.  
RL THIRION S., MONTAN R., HETZIGEN H., RAUS J., VANDEVYVER C.;  
INMODOGENETICS 43:167-168(1996).  
DR PNAS: P00047; 15.  
KW SIGNAL.

FT CHAIN 1 19 POTENTIAL.  
FT SIGNAL 20 152 ANTIEN, B-CELL RECEPTOR.  
SQ SEQUENCE 152 AA: 16517 MW; A5E9253 CRC32:

Query Match 8.5%: Score 10; DB 11; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 26 SLTSDSNVYR 33  
QY 104 SLTSDSNVYR 115

RESULT 12 PRELIMINARY: PRT: 98 AA.

ID 051113  
AC 051113  
DT 01-JUN-1998 (TREMBL:06, CREATED)  
DT 01-JUN-1998 (TREMBL:06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBL:06, LAST ANNOTATION UPDATE)  
DE ANTI-HV-1 REVERSE TRANSCRIPTASE SINGLE-CHAIN VARIABLE FRAGMENT.  
DE CCA-433 PRECURSOR (FRAGMENT).  
DE MUS MUSCULUS (MOUSE).  
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
OC EUKARYOTA: RODENTIA.  
RN 11  
RS SEQUENCE FROM N.A.  
RC STRAIN: BALB/C.  
RA MEDLINE: 96211469.  
RL SHAHREK F., DUAN L., SHU M., BAGASRA O., POKERANTZ R.J.;  
J. VIROL. 70:1392-1400(1996).  
DR PNAS: P00047; 15.  
KW SIGNAL.

FT CHAIN 1 19 POTENTIAL.  
FT SIGNAL 20 152 ANTIEN, B-CELL RECEPTOR.  
SQ SEQUENCE 152 AA: 16517 MW; A5E9253 CRC32:

Query Match 6.5%: Score 10; DB 11; Length 98;  
Best Local Similarity 90.9%; Pred. No. 1.92e-07;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 84 SELSDSNVYR 94  
QY 103 SELSDSNVYR 113

ID 035529 PRELIMINARY: PRT: 116 AA.  
 AC 035529: (REBUILT: 05, CREATED)  
 DT 01-JAN-1998 (REBUILT: 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (REBUILT: 05, LAST SEQUENCE UPDATE)  
 DE ANTI-ACID PROPHASE VARIABLE HEAVY CHAIN 12 (FRAGMENT)  
 OS MUS MUSCULUS (MUSC)  
 OC EUTHERIA: NEOTOMA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 116 116  
 FT SEQUENCE 116 AA: 11097 MW; 5875624 CIRC32;  
 Query Match 6.5% Score 10; DB 11; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-07;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 85 SLTSDSNV 94  
 QY 104 SLTSDSNV 113  
 RESULT 14 PRELIMINARY: PRT: 120 AA.  
 ID 035528  
 AC 035528: (REBUILT: 05, CREATED)  
 DT 01-JAN-1998 (REBUILT: 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (REBUILT: 05, LAST SEQUENCE UPDATE)  
 DE ANTI-ACID PROPHASE VARIABLE LIGHT CHAIN 11 (FRAGMENT)  
 OS MUS MUSCULUS (MUSC)  
 OC EUTHERIA: NEOTOMA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 120 120  
 FT SEQUENCE 120 AA: 13235 MW; 9041015 CIRC32;  
 Query Match 6.5% Score 10; DB 11; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-07;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 85 SLTSDSNV 94  
 QY 104 SLTSDSNV 113

OC EUTHERIA: RODENTIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 125 125  
 FT SEQUENCE 125 AA: 13544 MW; 9389000 CIRC32;  
 Query Match 6.5% Score 10; DB 11; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-07;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 4 LOGSALV 13  
 QY 23 LOGSALV 32  
 RESULT 17 PRELIMINARY: PRT: 249 AA.  
 ID 035527  
 AC 035527: (REBUILT: 05, CREATED)  
 DT 01-JAN-1998 (REBUILT: 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (REBUILT: 05, LAST SEQUENCE UPDATE)  
 DE ANTI-ACID PROPHASE VARIABLE HEAVY CHAIN 12 (FRAGMENT)  
 OS MUS MUSCULUS (MUSC)  
 OC EUTHERIA: NEOTOMA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 249 249  
 FT SEQUENCE 249 AA: 26839 MW; 4288042 CIRC32;  
 Query Match 6.5% Score 10; DB 11; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-07;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 4 LOGSALV 13  
 QY 23 LOGSALV 32

Query Match 6.5% Score 10; DB 11; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-07;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 85 SLTSDSNV 94  
 QY 104 SLTSDSNV 113  
 RESULT 15 PRELIMINARY: PRT: 123 AA.  
 ID 041218  
 AC 041218: (REBUILT: 01, CREATED)  
 DT 01-NOV-1996 (REBUILT: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (REBUILT: 01, LAST SEQUENCE UPDATE)  
 DE ANTI-ACID PROPHASE VARIABLE HEAVY CHAIN 12 (FRAGMENT)  
 OS MUS MUSCULUS (MUSC)  
 OC EUTHERIA: NEOTOMA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 123 123  
 FT SEQUENCE 123 AA: 13006 MW; 9041015 CIRC32;  
 Query Match 6.5% Score 10; DB 11; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-07;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 85 SLTSDSNV 94  
 QY 104 SLTSDSNV 113  
 RESULT 16 PRELIMINARY: PRT: 135 AA.  
 ID 041219  
 AC 041219: (REBUILT: 06, CREATED)  
 DT 01-JUN-1998 (REBUILT: 06, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (REBUILT: 06, LAST SEQUENCE UPDATE)  
 DE ANTI-ACID PROPHASE VARIABLE HEAVY CHAIN 12 (FRAGMENT)  
 OS MUS MUSCULUS (MUSC)  
 OC EUTHERIA: NEOTOMA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 135 135  
 FT SEQUENCE 135 AA: 13006 MW; 9041015 CIRC32;  
 Query Match 6.5% Score 10; DB 11; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-07;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 85 SLTSDSNV 94  
 QY 104 SLTSDSNV 113

QY 23 LOGSALV 32  
 RESULT 18 PRELIMINARY: PRT: 133 AA.  
 ID 031178  
 AC 031178: (REBUILT: 01, CREATED)  
 DT 01-NOV-1996 (REBUILT: 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (REBUILT: 01, LAST SEQUENCE UPDATE)  
 DE ANTI-ACID PROPHASE VARIABLE HEAVY CHAIN 12 (FRAGMENT)  
 OS MUS MUSCULUS (MUSC)  
 OC EUTHERIA: NEOTOMA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 133 133  
 FT SEQUENCE 133 AA: 13124 MW; 5106007 CIRC32;  
 Query Match 5.9% Score 9; DB 7; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 4.12e-05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 101 EDNAVYCA 109  
 QY 108 EDNAVYCA 116  
 RESULT 19 PRELIMINARY: PRT: 98 AA.  
 ID 041222  
 AC 041222: (REBUILT: 06, CREATED)  
 DT 01-JUN-1998 (REBUILT: 06, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (REBUILT: 06, LAST SEQUENCE UPDATE)  
 DE ANTI-ACID PROPHASE VARIABLE HEAVY CHAIN 12 (FRAGMENT)  
 OS MUS MUSCULUS (MUSC)  
 OC EUTHERIA: NEOTOMA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAL/C:  
 RA TAKAHASHI, K. MITAKOTO T., SOEDA T., SAKAMOTO J., MITAKOTO T.,  
 RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DDJ DATA BANKS.  
 DR EMBL: D50137; D1024480; ..  
 DR PRN: P00047; 19; ..  
 FT NON-TER 98 98  
 FT SEQUENCE 98 AA: 10606 MW; 5106007 CIRC32;  
 Query Match 5.9% Score 9; DB 7; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 4.12e-05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 101 EDNAVYCA 109  
 QY 108 EDNAVYCA 116

MOI: INTRONL 0.0-0.1997)  
 DR EMIL: AF035786; G2655850;  
 FT NON\_TER 1 1  
 SQ SEQUENCE 98 AA: 10912 MW: 4F9C1186 CRC32: ---  
 Query Match 5.2%: Score 8; DB 4; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSITT 28  
 CY 40 SCANSITT 47  
 RESULT 20  
 ID 099824 PRELIMINARY: PRT: 124 AA.  
 AC 099824 (REPROBABLE, 03, CREATED)  
 DT 01-MAY-1997 (REPROBABLE, 03, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (REPROBABLE, 06, LAST ANNOTATION UPDATE)  
 DE ANTI-HIV-1 G2120 ANTIBODY P35 HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUTHERIA: PRIMATES.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BONE-MARROW; P.M.N.I., BINKLEY J.M., SODROSKI J., MOORE J.P.,  
 RA BARBAS C.F., BURTON D.B.,  
 DR EMIL: D827711.G1785876;  
 DR PPM: P00047; 19. 124  
 SQ SEQUENCE 124 AA: 13450 MW: E8F13C00 CRC32: ---

Query Match 5.2%: Score 8; DB 4; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 106 LDYMOGT 113  
 CY 124 LDYMOGT 111  
 RESULT 21  
 ID 099826 PRELIMINARY: PRT: 125 AA.  
 AC 099826 (REPROBABLE, 03, CREATED)  
 DT 01-MAY-1997 (REPROBABLE, 03, LAST SEQUENCE UPDATE)  
 DE 01-MAY-1997 (REPROBABLE, 03, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (REPROBABLE, 06, LAST ANNOTATION UPDATE)

FT CHAIN 20 >112 POTENTIAL.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 132 AA: 14674 MW: 9364D0DD CRC32: ---  
 Query Match 5.2%: Score 8; DB 7; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 103 DSATYCA 110  
 CY 109 DSATYCA 116  
 RESULT 23  
 ID 099771 PRELIMINARY: PRT: 241 AA.  
 AC 099771 (REPROBABLE, 03, CREATED)  
 DT 01-MAY-1997 (REPROBABLE, 03, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (REPROBABLE, 06, LAST ANNOTATION UPDATE)  
 DE ANTI-CD4 79 SINGLE CHAIN PV FRAGMENT (FRAGMENT).  
 OS EUTHERIA: RODENTIA.  
 OC EUTHERIA: RODENTIA.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC KIM I.J., CHOI I.H., CHUNG H.K.,  
 RA KIM I.J., CHOI I.H., CHUNG H.K.,  
 DR EMIL: D88087.G1850548;  
 DR PPM: P00047; 19. 1  
 FT NON\_TER 241 241  
 SQ SEQUENCE 241 AA: 26086 MW: E8B2D29D CRC32: ---

Query Match 5.2%: Score 8; DB 11; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSITT 28  
 CY 40 SCANSITT 47  
 RESULT 24  
 ID 0990288 PRELIMINARY: PRT: 244 AA.  
 AC 0990288 (REPROBABLE, 04, CREATED)  
 DT 01-JUL-1997 (REPROBABLE, 04, LAST SEQUENCE UPDATE)  
 DE 01-JUL-1997 (REPROBABLE, 04, LAST SEQUENCE UPDATE)  
 DE SINGLE-CHAIN PV FRAGMENT (FRAGMENT).  
 GN SCV.

DE PLATELET MEMBRANE GLYCOPROTEIN IB (CD1B) SPECIFIC ANTIBODY (FRAGMENT).  
 GN 11-02  
 OS HOMO SAPIENS (HUMAN).  
 OC EUTHERIA: PRIMATES.  
 OC EUTHERIA: PRIMATES.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE: 91370594.  
 RA HIRATAVA A., NGUYEN D.J., MILLER E.C.;  
 DR EMIL: D810711.G1071151990;  
 DR PPM: P00047; 19. 1  
 FT NON\_TER 125 125  
 SQ SEQUENCE 125 AA: 13722 MW: 857E85A CRC32: ---

Query Match 5.2%: Score 8; DB 4; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSITT 28  
 CY 40 SCANSITT 47  
 RESULT 22  
 ID 031177 PRELIMINARY: PRT: 132 AA.  
 AC 031177 (REPROBABLE, 01, CREATED)  
 DT 01-NOV-1996 (REPROBABLE, 01, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (REPROBABLE, 06, LAST ANNOTATION UPDATE)  
 DE NRC CLASS II I-A-ALPHA mRNA  
 DE (H-2B). 5' END. HYBRIDOMA AF.3.C7 PRECURSOR (FRAGMENT).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUTHERIA: RODENTIA.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC J. HONIGSMAN, J. HONIGSMAN T.H., WALSH M.D., BENITE M.A., TILLINGHAST J.P.,  
 RA CHOW H.S., WHITLEY P.J., KAPP J.A., PIERCE C.W., SIEVACH E.M.,  
 DR EMIL: D81518.G194600;  
 DR PPM: P00047; 19. 1  
 FT SIGNAL 1 19 POTENTIAL.

OS HOMO SAPIENS (HUMAN).  
 OC EUTHERIA: PRIMATES.  
 OC EUTHERIA: PRIMATES.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC ROYERMAN R.R., WING M.G., WINTER C.;  
 DR EMIL: D11057.G112725;  
 DR PPM: P00047; 19. 1  
 FT NON\_TER 244 244  
 SQ SEQUENCE 244 AA: 26127 MW: ACF148B CRC32: ---

Query Match 5.2%: Score 8; DB 4; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSITT 28  
 CY 40 SCANSITT 47  
 RESULT 25  
 ID 015224 PRELIMINARY: PRT: 38 AA.  
 AC 015224 (REPROBABLE, 05, CREATED)  
 DT 01-JUN-1998 (REPROBABLE, 05, LAST SEQUENCE UPDATE)  
 DE 01-JUN-1998 (REPROBABLE, 05, LAST SEQUENCE UPDATE)  
 DE CD3-IGG (FRAGMENT).  
 OS HOMO SAPIENS (HUMAN).  
 OC EUTHERIA: PRIMATES.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC OTTENHEIMER C.H., STENSON F.A.;  
 RA OTTENHEIMER C.H., STENSON F.A.;  
 DR EMIL: A000411.E339711;  
 DR PPM: P00047; 19. 1  
 FT NON\_TER 38 38  
 SQ SEQUENCE 38 AA: 4355 MW: 37E8917 CRC32: ---



01-MAY-1997 (TREMBL, 03, CREATED)  
 DT 01-MAY-1997 (TREMBL, 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)  
 DE AVI-HIV-1 GP120 ANTIBODY P7 HEAVY CHAIN VARIABLE REGION (FRAGMENT)  
 OS HOMO SAPIENS (HUMAN)  
 OC CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 CC EUTHERIA: PRIMATES  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: BONE-MARROW  
 RC CELL: B-LYMPHOCYTE  
 RA BARBAS C.P., BURTON D.R.,  
 RL SUBMITTED (DEC-1996) TO ENGL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: 082767; GI785681;  
 RN PRN: P00047; 19;  
 FT NON-TER 136 136  
 SO SEQUENCE 136 AA: 14644 MW: 350424.6 CRC32:  
 Query Match 4.64: Score 7; DB 4; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 39 POCLEIN 45  
 CY 60 DYWGCGT 66  
 RESULT 34 PRELIMINARY: PRT: 143 AA.  
 ID Q93647;  
 AC Q93647;  
 DT 01-JAN-1998 (TREMBL, 05, CREATED)  
 DT 01-JAN-1998 (TREMBL, 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)  
 DE HYPHOSIN, 15.9 KD PROTEIN.  
 OS MYCOBACTERIUM LEPRAE  
 OC PROKARYOTA: BACTERIA: ACTINOMYCETES: MYCOBACTERIACEAE.  
 CC SEQUENCE FROM N.A.  
 RC BACCOCK K., CROCHER C.H.;  
 RL SUBMITTED (SEP-1997) TO ENGL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: 082767; GI785681;  
 RN PRN: P00047; 19;  
 FT NON-TER 136 136  
 SO SEQUENCE 136 AA: 14644 MW: 350424.6 CRC32:  
 Query Match 4.64: Score 7; DB 4; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 39 POCLEIN 45  
 CY 60 DYWGCGT 66

DE (FRAGMENT).  
 CN VACCINIA  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 CC EUTHERIA: PRIMATES  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE: 51370594  
 RA HIRATA A., NGUYEN D.J., MILLER E.C.;  
 RL AUTOIMMUNITY 8:107-113(1990).  
 DR EMBL: 086531; GI181666;  
 RN PRN: P00047; 19;  
 FT SIGNAL 1 19  
 FT CHAIN 20 >148  
 FT NON-TER 148 148  
 SO SEQUENCE 148 AA: 16479 MW: 3882346 CRC32:  
 Query Match 4.64: Score 7; DB 4; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 136 DYWGCGT 142  
 CY 135 DYWGCGT 131  
 RESULT 37 PRELIMINARY: PRT: 198 AA.  
 ID Q93647;  
 AC Q93647;  
 DT 01-JUN-1997 (TREMBL, 04, CREATED)  
 DT 01-JUN-1997 (TREMBL, 04, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1997 (TREMBL, 04, LAST ANNOTATION UPDATE)  
 DE HOMO SAPIENS (HUMAN)  
 OC CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 CC EUTHERIA: PRIMATES  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC DODDLEA P.K., BAO D.D., STEY I., JOSEPH V., DANIEL R.Y., GARDNER C.,  
 RA RISK M.C., SCHWARTZ D., BAYSHI D., KIM K.E., HARTO J.M.,  
 RA GOLDSTEIN J.L., LAYDEN T.J., RAMANATHAN K.;  
 DR EMBL: 081450; GI111725;  
 RN PRN: P00047; 19;  
 FT NON-TER 198 198  
 SO SEQUENCE 198 AA: 22957 MW: 5137056 CRC32:

DR EMBL: 081450; GI111725;  
 RN PRN: P00047; 19;  
 SO SEQUENCE 198 AA: 22957 MW: 5137056 CRC32:  
 Query Match 4.64: Score 7; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 96 GSAELV 102  
 CY 25 GSAELV 31  
 RESULT 35 PRELIMINARY: PRT: 147 AA.  
 ID Q13647;  
 AC Q13647;  
 DT 01-NOV-1996 (TREMBL, 01, CREATED)  
 DT 01-NOV-1996 (TREMBL, 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBL, 01, LAST ANNOTATION UPDATE)  
 DE V1316 HEAVY CHAIN VARIABLE REGION (CDR1 TO CDR3 REGIONS (FRAGMENT)).  
 OS HOMO SAPIENS (HUMAN)  
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 CC EUTHERIA: PRIMATES  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE: 56071449  
 RA CAO J., VESICIO R.A., NETTIO M.B., HONG C.H., KIM A., LEE J.C.,  
 RA LICHTENSTEIN A.K., BERENSON J.R.;  
 DR EMBL: 080860; GI244581;  
 RN PRN: P00047; 19;  
 FT NON-TER 147 147  
 SO SEQUENCE 147 AA: 15768 MW: 350424.6 CRC32:  
 Query Match 4.64: Score 7; DB 4; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 114 DYWGCGT 120  
 CY 125 DYWGCGT 131  
 RESULT 36 PRELIMINARY: PRT: 148 AA.  
 ID Q93647;  
 AC Q93647;  
 DT 01-MAY-1997 (TREMBL, 03, CREATED)  
 DT 01-MAY-1997 (TREMBL, 03, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)  
 DE PLATELET MEMBRANE GLYCOPROTEIN IS (GP1B) SPECIFIC ANTIBODY PRECURSOR

Query Match 4.64: Score 7; DB 4; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 114 SLNDYTS 120  
 CY 88 SLNDYTS 94  
 RESULT 38 PRELIMINARY: PRT: 251 AA.  
 ID Q43306;  
 AC Q43306;  
 DT 01-JUN-1998 (TREMBL, 05, CREATED)  
 DT 01-JUN-1998 (TREMBL, 05, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)  
 DE CAENORHABDITIS ELEGANS.  
 OS EUKARYOTA: METAZOA: ACCELLOMATES: NEMATODA: SECERNENTYEA: RHABDITIDA.  
 CC SEQUENCE FROM N.A.  
 RC [1]  
 RP SEQUENCE FROM N.A.  
 RC [1]  
 RL SUBMITTED (JAN-1997) TO ENGL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: 081450; GI111725;  
 RN PRN: P00047; 19;  
 FT NON-TER 251 251  
 SO SEQUENCE 251 AA: 4298845 CRC32:  
 Query Match 4.64: Score 7; DB 5; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 53 PFLTST 59  
 CY 7 PFLTST 13  
 RESULT 39 PRELIMINARY: PRT: 299 AA.  
 ID Q41653;  
 AC Q41653;



```

OC MUS MUSCULUS (MUSCULUS)
OC EUMYRTOGA METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUMYRTOGA: RODENTIA:
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 98070772.
RA COHEN-SALMON M., EL-AMRADI A., LEBOVICI M., PETIT C.,
DR PROC. NATL. ACAD. SCI. U.S.A. 94:1450-1455(1997).
SQ SEQUENCE: 2910 AA: 313410 MW: 9456568 CRC32:
Query Match 4.6%; Score 7; DB 11; Length 2910;
Best Local Similarity 100.0%; Pred. No. 7.10e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 676 PLVPSI: 682
CY 147 PLVPSI: 153
RESULT 46
ID P78465 PRELIMINARY: PRT: 12 AA.
AC G01054;
DT 01-NOV-1996 (TREMBL:EL. 03, CREATED)
DT 01-NOV-1997 (TREMBL:EL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (TREMBL:EL. 03, LAST SEQUENCE UPDATE)
DE POLYCLONAL LYMPHOMA T(14;18) CHROMOSOMAL TRANSLOCATION JUNCTION.
OC EUMYRTOGA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUMYRTOGA: PRIMATES:
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 98070772.
RA COHEN-SALMON M., EL-AMRADI A., LEBOVICI M., PETIT C.,
DR PROC. NATL. ACAD. SCI. U.S.A. 94:1450-1455(1997).
SQ SEQUENCE: 12 AA: 1297 MW: 1993244 CRC32:
Query Match 3.9%; Score 6; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.74e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 YNOCOT 6
CY 126 YNOCOT 131
RESULT 47
ID Q78986 PRELIMINARY: PRT: 28 AA.
AC Q78986;
DB 1 YNOCOT 6
CY 126 YNOCOT 131
```

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DB 7 FLPLIS 12
CY 7 FLPLIS 12
RESULT 49
ID Q18715 PRELIMINARY: PRT: 56 AA.
AC Q18715;
DT 01-JAN-1998 (TREMBL:EL. 05, CREATED)
DT 01-JAN-1998 (TREMBL:EL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBL:EL. 05, LAST SEQUENCE UPDATE)
DE CYSTEINE PROTEASE (FRAGMENT).
OC EUTIMOBIA DISPAR.
OC EUTIMOBIA: KITCHENORIAL: EUTIMOBIA: EUTIMOBIA: EUTIMOBIA.
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN-SAV 142;
RA BHATTACHARYA A., SHARMA R., ANAN A., BHATTACHARYA S.,
DR EMBO J. 14(1997) 7225-7230; DOI:10.1093/emboj/cda142.
SQ SEQUENCE: 56 AA: 6341 MW: 6218687 CRC32:
Query Match 3.9%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.74e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 21 NREFG 26
CY 80 NREFG 85
RESULT 50
ID Q41401 PRELIMINARY: PRT: 64 AA.
AC Q41401;
DT 01-NOV-1996 (TREMBL:EL. 01, CREATED)
DT 01-NOV-1996 (TREMBL:EL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBL:EL. 01, LAST SEQUENCE UPDATE)
DE EARLY NODULIN (EMO2-3A) PROTEIN (FRAGMENT).
OC SENSILLA ROSHATA.
OC SENSILLA: PLANTIA: EMBRYOPHTHA: ANGIOSPERMAE: DICOTYLEDONEAE: FRALAE:
OC FRALAE:
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN-SAV 142;
RA BHATTACHARYA A., SHARMA R., ANAN A., BHATTACHARYA S.,
DR EMBO J. 14(1997) 7225-7230; DOI:10.1093/emboj/cda142.
SQ SEQUENCE: 64 AA: 7356 MW: 3721390 CRC32:
Query Match 3.9%; Score 6; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.74e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 3 PPVYP 8
CY 142 PPVYP 147
```

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DB 3 PPVYP 8
CY 142 PPVYP 147
Search completed: Thu Apr 15 18:10:46 1999
Job time : 77 sec.
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DT 01-NOV-1996 (TREMBL:EL. 01, CREATED)
DT 01-NOV-1996 (TREMBL:EL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBL:EL. 01, LAST SEQUENCE UPDATE)
DE HEAVY-CHAIN COMPLEMENTABILITY-DETERMINING REGION 3 RNA
OC (CLONE 22), PARTIAL CDS (FRAGMENT).
OC HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 92052122.
RA BERNARD C.F. III, PERSSON M.A., KOENIG S., CHANOK R.M.,
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 28 AA: 3226 MW: 3586005 CRC32:
Query Match 3.9%; Score 6; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.74e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 23 DYWOC 28
CY 125 DYWOC 130
RESULT 48
ID G01054 PRELIMINARY: PRT: 54 AA.
AC G01054;
DT 01-NOV-1996 (TREMBL:EL. 01, CREATED)
DT 01-NOV-1996 (TREMBL:EL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBL:EL. 01, LAST SEQUENCE UPDATE)
DE KUTYRONCES LACTIS (TBA87).
OC KUTYRONCES LACTIS (TBA87).
OC PLASMID KL.
OC EUMYRTOGA: FUNGI: ASCOMYCOTINA: HEMIASCOCETES.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 87004569.
RA STARK M.J.R., BOLD A.,
DR EMBO J. 5:1195-1200(1986).
SQ SEQUENCE: 54 AA: 6435 MW: 8858990 CRC32:
Query Match 3.9%; Score 6; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.74e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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971	6	3.9	348	J6211	interferon receptor- $\alpha$	1.15+02
972	6	3.9	352	B1166	probable peptide cist	1.15+02
973	6	3.9	353	B1166	beta-2 glucanase	1.15+02
974	6	3.9	364	C4874	mannan 6-phosphatase	1.15+02
975	6	3.9	382	D2058	manno protein - fucose	1.15+02
976	6	3.9	403	D	hypothetical protein	1.15+02
977	6	3.9	403	D	hypothetical protein	1.15+02
978	6	3.9	414	D	probable reov protein	1.15+02
979	6	3.9	414	D	probable reov protein	1.15+02
980	6	3.9	442	A1733	apolipoprotein A-I re	1.15+02
981	6	3.9	442	A1733	apolipoprotein A-I re	1.15+02
982	6	3.9	442	H0481	hemolysin homolog pro	1.15+02
983	6	3.9	442	C6414	beta-2 glucanase (PC	1.15+02
984	6	3.9	440	D	hypothetical 51.6K pr	1.15+02
985	6	3.9	440	D	probable transacetyllo	1.15+02
986	6	3.9	512	C0161	glycoprotein recepto	1.15+02
987	6	3.9	529	D	glycoprotein recepto	1.15+02
988	6	3.9	532	A1333	spenn surface protein	1.15+02
989	6	3.9	544	D	neuroglycan C precursor	1.15+02
990	6	3.9	561	D	kringle protein glass	1.15+02
991	6	3.9	766	D	hypothetical 72.8 kD	1.15+02
992	6	3.9	766	D	hypothetical 72.8 kD	1.15+02
993	6	3.9	85764	B5164	ethanol(1)malignant b	1.15+02
994	6	3.9	87478	D	nonhuman protein S1	1.15+02
995	6	3.9	87478	D	nonhuman protein S1	1.15+02
996	6	3.9	87478	D	nonhuman protein S1	1.15+02
997	6	3.9	84087	D	serotonine-10m re	1.15+02
998	6	3.9	874450	D	acetateoxazin binding p	1.15+02
999	6	3.9	871156	D	receptor-protein tyro	1.15+02
1000	6	3.9	1230	D	hypothetical protein	1.15+02
			1407	D	hypothetical protein	1.15+02
			853934	D	DNA-directed RNA polyn	1.15+02

[illegible]

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[illegible]

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#sequence
#reference Q3:193100; CB:1070794; MID:951591; PID:9310150
#clone
#description This is an anti-idiotypic antibody from A/J mice
#antigen Immunized with anti-phenolase antibodies (also from A/J
#mice)
#sequences from two other clones (18628-16 and 12684-3)
#sequence identical to that shown: residue 48 vs
#heteroepitope Immunoglobulin V region; Immunoglobulin homology
heteroepitope: Immunoglobulin
#length 119 molecular weight 11228 kDa
#sequence 992
#analysis
#analysis 14-4% Score 22; db 2; length 119;
#analysis best local similarity 100.0%; Pval. No. 6,586-13;
#analysis Matches 221 Conservative 0; Miscellaneous 0; Gaps 0;
#analysis Db 73 DDBSNANQ151STREDAVY 94
#analysis |||||||
#analysis QY 92 DDBSNANQ151STREDAVY 113

#RESULT 2
#ENTRY
#protein
#organism
#date
#accessions
#keywords
#database
#comments
#sequence
#residues
#aminoacids
#molecular_type RNA
#notes
#experimental_source cell line ccl1
#notes This protein is an anti-idiotypic antibody that induces an
#notes superinduced immunoglobulin V region; Immunoglobulin homology
#notes heteroepitope: Immunoglobulin
#classification
#keywords
#remarks
#features
#sequence
#analysis
#analysis 50-54
#analysis 65-83

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[illegible]

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9861	27	6.2	160.29	MORC1D	Mouse musculus	Immuno	1.82e-07
9862	27	6.2	160.29	MORC1A	Mouse sp. active	Asp	1.82e-07
9863	27	6.2	160.29	MORC1B	Mouse musculus	Immuno	1.82e-07
9864	27	6.2	160.29	MORC1C	Mouse musculus	Immuno	1.82e-07
9865	27	6.2	160.29	MORC1D	Mouse musculus	Immuno	1.82e-07
9866	27	6.2	160.29	MORC1E	Mouse musculus	Immuno	1.82e-07
9867	27	6.2	160.29	MORC1F	Mouse musculus	Immuno	1.82e-07
9868	27	6.2	160.29	MORC1G	Mouse musculus	Immuno	1.82e-07
9869	27	6.2	160.29	MORC1H	Mouse musculus	Immuno	1.82e-07
9870	27	6.2	160.29	MORC1I	Mouse musculus	Immuno	1.82e-07
9871	27	6.2	160.29	MORC1J	Mouse musculus	Immuno	1.82e-07
9872	27	6.2	160.29	MORC1K	Mouse musculus	Immuno	1.82e-07
9873	27	6.2	160.29	MORC1L	Mouse musculus	Immuno	1.82e-07
9874	27	6.2	160.29	MORC1M	Mouse musculus	Immuno	1.82e-07
9875	27	6.2	160.29	MORC1N	Mouse musculus	Immuno	1.82e-07
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9882	27	6.2	160.29	MORC1U	Mouse musculus	Immuno	1.82e-07
9883	27	6.2	160.29	MORC1V	Mouse musculus	Immuno	1.82e-07
9884	27	6.2	160.29	MORC1W	Mouse musculus	Immuno	1.82e-07
9885	27	6.2	160.29	MORC1X	Mouse musculus	Immuno	1.82e-07
9886	27	6.2	160.29	MORC1Y	Mouse musculus	Immuno	1.82e-07
9887	27	6.2	160.29	MORC1Z	Mouse musculus	Immuno	1.82e-07
9888	27	6.2	160.29	MORC1A	Mouse musculus	Immuno	1.82e-07
9889	27	6.2	160.29	MORC1B	Mouse musculus	Immuno	1.82e-07
9890	27	6.2	160.29	MORC1C	Mouse musculus	Immuno	1.82e-07
9891	27	6.2	160.29	MORC1D	Mouse musculus	Immuno	1.82e-07
9892	27	6.2	160.29	MORC1E	Mouse musculus	Immuno	1.82e-07
9893	27	6.2	160.29	MORC1F	Mouse musculus	Immuno	1.82e-07
9894	27	6.2	160.29	MORC1G	Mouse musculus	Immuno	1.82e-07
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9897	27	6.2	160.29	MORC1J	Mouse musculus	Immuno	1.82e-07
9898	27	6.2	160.29	MORC1K	Mouse musculus	Immuno	1.82e-07
9899	27	6.2	160.29	MORC1L	Mouse musculus	Immuno	1.82e-07
9900	27	6.2	160.29	MORC1M	Mouse musculus	Immuno	1.82e-07
9901	27	6.2	160.29	MORC1N	Mouse musculus	Immuno	1.82e-07
9902	27	6.2	160.29	MORC1O	Mouse musculus	Immuno	1.82e-07
9903	27	6.2	160.29	MORC1P	Mouse musculus	Immuno	1.82e-07
9904	27	6.2	160.29	MORC1Q	Mouse musculus	Immuno	1.82e-07
9905	27	6.2	160.29	MORC1R	Mouse musculus	Immuno	1.82e-07
9906	27	6.2	160.29	MORC1S	Mouse musculus	Immuno	1.82e-07
9907	27	6.2	160.29	MORC1T	Mouse musculus	Immuno	1.82e-07
9908	27	6.2	160.29	MORC1U	Mouse musculus	Immuno	1.82e-07
9909	27	6.2	160.29	MORC1V	Mouse musculus	Immuno	1.82e-07
9910	27	6.2	160.29	MORC1W	Mouse musculus	Immuno	1.82e-07
9911	27	6.2	160.29	MORC1X	Mouse musculus	Immuno	1.82e-07
9912	27	6.2	160.29	MORC1Y	Mouse musculus	Immuno	1.82e-07
9913	27	6.2	160.29	MORC1Z	Mouse musculus	Immuno	1.82e-07
9							

RESULT	1	RD	01-NOV-1991
LOCUS			
DEFINITION	MUSICLAVY 301 bp mRNA		
ACCESSION	Mouse Ig kappa-chain mRNA V region, partial cds, from hybridoma H20-23.		
KEYWORDS	M86246		
FEATURES	5187531		
DESCRIPTION	V-region: immunoglobulin kappa-chain: immunoglobulin light chain		

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QY	263	ATGCGACCTTCAATCTGAAATATTCCTAACCCATATCTCTGTCAATCAATACCTGATCTCT	342
DB	265	CGTTCGACCTGCTGACGAGGAGGACACGACCTGCTGATTTTAAAA	303
QY	343	CGGCAACGCTGTGGAGGAGGAGGACACGACCTGCTGATTTTAAAA	361
REFERENCE	2	MDG5588	307 bp mRNA
LOCUS			RGD
DEFINITION		mus musculus anti-DNA immunoglobulin light chain 150, antibody	06-MAR-1987
ACCESSION		U01587	partial cds.
KEYWORDS		g1870291	
SOURCE		house mouse	
ORGANISM		Mus musculus	
		Poliovirus; altheoviral; eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;	
		Mus (base 1 to 302)	
REFERENCE	1	Kirihara N.R., Jon X.-T. and Marlow T.R. "v-crb3 structures and	
LOCUS		correlation between somatically derived v-crb3 antibodies to DNA	
TITLE		spectrally (1987) in press	
JOURNAL		2. (base 1 to 303)	
AUTHORS		Marlow, T.R.	
REFERENCE		Direct submission	
TITLE		U01588(1986) Tony N. Marlow, Dept. of	
LOCUS		Immunobiology/Immunology, University of Tennessee, 618 Madison Ave.,	
DEFINITION		Knoxville, TN 37933, USA	
ACCESSION			
KEYWORDS		Location/Qualifiers	
SOURCE		1. (base 1 to 303)	
ORGANISM		Mus musculus	

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CDS           <I..>.302
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              /db_xref="pmid:1707923"
              /definition="KATSPESLILASLCSEYFETNADAGSGSTPRTIRH
              IATSLDLSCSYRHSRSGSDSRITSLRLSLSRGGPTCLTSLAPFTTCGGCTLL

```

```
Query Match      JJ 89 score 147, DB 29, length 303;
Best Local Similarity 99.0% Pred. No. 1.17e+14!
.....other .. vndn= 0. Gams 0
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[illegible][illegible]

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[illegible]

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not generated.

1 MECSWVFLFLSITTVHSQ.....TVSSAKTTPPPVYPLVPSL 153

## Gap 11

116695 seqs, 37453910 residues

Listing first 45 summarless

1:plr1 2:plr2 3:plr3 4:plr4

Mean 42.120; Variance 104.479; scale 0.403

ived by analysis of the total score distribution.

## SUMMARIES

It	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	783	70.6	475	2	S01321	Ig gamma-2b chain pre	4,38e-11
2	780	70.3	474	2	S25057	Ig gamma-2b chain - m	1.38e-11
3	774	69.8	469	2	S37483	Ig gamma-2a chain - m	1.37e-11
4	767	69.2	151	1	PJ0011	Ig heavy chain precur	2.00e-11
5	763	68.8	150	2	PN0444	Ig heavy chain V regl	9.24e-11
6	746	67.3	139	2	PS0024	Ig heavy chain precur	6.10e-11
7	742	66.9	166	2	PL0012	Ig heavy chain precur	2.81e-99
8	727	65.6	137	2	H32513	Ig heavy chain precur	8.57e-99
9	724	65.3	246	2	S38950	Ig gamma chain - mous	2.69e-96
10	724	65.3	446	2	S40295	Ig gamma-2a chain - mous	2.69e-96
11	710	64.0	178	2	S25954	Ig gamma chain (NM65)	5.57e-99
12	709	63.9	140	1	HWMSG7	Ig heavy chain precur	8.15e-99
13	705	63.8	138	2	S21810	Ig heavy chain V regl	1.19e-99
14	697	63.6	140	2	PH1482	Ig heavy chain V regl	3.74e-99
15	697	62.8	140	2	PH1489	Ig heavy chain V regl	7.84e-99
16	692	62.4	138	2	E32512	Ig heavy chain precur	5.25e-99
17	666	61.9	140	2	PH1488	Ig heavy chain V regl	5.13e-99
18	665	61.8	136	2	PL0208	Ig heavy chain precur	7.50e-99
19	664	61.7	141	2	A39276	Ig heavy chain precur	1.10e-98
20	661	61.4	140	2	PH1484	Ig heavy chain V regl	3.43e-88
21	678	61.1	139	2	A27607	Ig heavy chain precur	1.07e-88
22	676	61.0	135	2	A20579	Ig heavy chain precur	2.29e-88
23	675	60.9	135	2	PS0057	Ig heavy chain precur	3.34e-88

24	672	60.6	140	2	PH1498	Ig heavy chain V reg1	3.34e-88
25	675	60.6	135	2	PH1493	Ig heavy chain V reg1	1.04e-87
26	671	60.5	137	2	PH1227	Ig heavy chain precut	1.53e-87
27	670	60.4	135	2	PH1494	Ig heavy chain V reg1	2.23e-87
28	670	60.4	135	2	PH1492	Ig heavy chain V reg1	2.23e-87
29	668	60.2	140	2	PH1486	Ig heavy chain V reg1	4.76e-87
30	664	59.9	140	2	PH1483	Ig heavy chain V reg1	2.17e-88
31	661	59.6	117	2	PC3289	Ig heavy chain precut	6.77e-88
32	661	59.6	133	2	PC3155	Ig heavy chain precut	6.77e-88
33	661	59.6	140	2	PC1819	Ig heavy chain V reg1	2.11e-88
34	655	59.1	139	1	JHMS18	Ig heavy chain precut	6.58e-88
35	653	58.9	141	2	JF20076	Ig heavy chain precut	1.40e-88
36	651	58.7	137	2	E29380	Ig heavy chain precut	2.99e-88
37	650	58.6	137	2	E29380	Ig heavy chain precut	4.37e-88
38	645	58.2	117	1	JHMS41	Ig heavy chain precut	2.90e-88
39	645	58.2	136	2	S04576	Ig heavy chain precut	2.90e-88
40	642	57.9	131	2	A27472	Ig heavy chain precut	9.03e-88
41	642	57.9	140	2	S04575	Ig heavy chain precut	9.03e-88
42	637	57.4	136	2	B47159	Ig heavy chain V reg1	5.98e-88
43	636	57.3	117	1	JHMS84	Ig heavy chain precut	8.73e-88
44	635	57.3	137	1	GHMS43	Ig heavy chain precut	1.27e-88
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## ALIGNMENTS

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ENTRY      1
TITLE      S01321      #type complete
ORGANISM   Ig gamma-2b chain precursor - mouse
DATE       $format_name Mus musculus #common_name house mouse
          30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change
          08-Sep-1997

ACCESSIONS
REFERENCE   S01321
AUTHORS    de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.;
          Piers, W.
          Eur. J. Biochem. (1988) 176:287-295
          Expression in non-lymphoid cells of mouse recombinant
          immunoglobulin directed against the tumour marker human
          placental alkaline phosphatase.
          #cross_references MIMD:88329081
          #accession      S01321
          #molecule_type mRNA
          #residues       1-475 ##label DE1
          #crosrefs       EMBL:X13186; NID:951780; PID:951781
          #note           this sequence was determined from the differenciated
                           gene
CLASSIFICAT
KEYWORDS    #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE     immunoglobulin
          1-19
          20-475      #domain signal sequence #status predicted #label SIG
          159-223      #domain immunoglobulin homology #label IG1
          #length 475 #molecular_weight 51567 #checksum 4130
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Best Local Similarity 71.4%; Pred. No. 4,38e-106;
Matches 110; Conservative 22; Mismatches 18; Indels 4; Gaps 3;

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1 MEWTWIFLILSTGAYQSOVQLQSGAGELIARPGASVKLSCKASGYTLTSGISNWKRT 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
20-475 1 MECSMVFILFLISTTGYSQAYVQLQSGAGELIYRSGAVSKSCASGYTLTSGNHHVKT 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY      61 GGGLEWIGETIYPGSGNENFEKRGKATLTIVKSSSTALHLSLTSSEDSAYFCFA- 119
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OY      61 GGGLEWIGNITFGNGDITITNOKFKGASLTADTSSSTAIHQISSLTSEDSAYFCARGW 120
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Db      120 QVGLLPFGYWGQGLTVYASAKTTPSPVYPLAG 153
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY      121 E-GAL--DYWGQGTSTVSSAKTTTPPVYPLVPG 151
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT      2

```

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QY 181 GGACAGGGGCTGGAATGATTTGGAATATTTTCTGGAATGATGATCTACTACAT 240  
 DB 279 CAGAGTTCAAGGCGCAAGCCCACTGACTGATGAGCAATCTCCAGCAGACCTACATG 338  
 QY 241 CAGAGTTCAAGGCGCAAGCCCTCATGACTGAGCAGACATCTCCAGCAGACCTACATG 300  
 DB 339 CAGCTCAGACGCTGACATCTGAGACTCTGCGGTCTATTTCTGTGCAAG 390  
 QY 301 CAGATCAGACGCTGACATCTGAGACTCTGCGGTCTATTTCTGTGCAAG 352

RESULT 2  
 LOCUS MUSIGHX 458 bp mRNA ROD 26-MAR-1994  
 DEFINITION Mouse Ig rearranged H-chain V-region mRNA VJ1.  
 ACCESSION M1953  
 NID 9196223  
 KEYWORDS C-region; V-region; immunoglobulin heavy chain; processed gene.  
 SOURCE Mus musculus cDNA to mRNA.  
 ORGANISM Mus musculus  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.  
 1 (bases 1 to 458)  
 Liu, A.Y., Robinson, R.R., Murray, E.D. Jr., Ledbetter, J.A., Hellstrom, I. and Hellstrom, K.E.  
 Production of a mouse-human chimeric monoclonal antibody to CD20 with potent FC-dependent biologic activity  
 J. Immunol. 139, 3521-3526 (1987)  
 MEDLINE 8806045  
 COMMENT Draft entry and computer-readable sequence [1] kindly submitted by A.Y. Liu, 02-FEB-1987.  
 FEATURES  
 source Location/Qualifiers  
 1..458  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /cell\_line="2H7"  
 39..>458  
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 /db\_xref="PID:9196224"  
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 410..411  
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 /organism="Mus musculus"

BASE COUNT 113 a 121 c 111 g 113 t  
 ORIGIN  
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 Best Local Similarity 94.6%; Pred. No. 2,71e-216;  
 Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 DB 39 ATGGATTAGAGATCTTCTCTCTCTCTGTCAGTACTACAGGTGTCACATCCAG 98  
 QY 1 ATGGATGAGCTGGGTCTTCTCTCTCTCTGTCATATACAGGTGTCACATCCAG 60  
 DB 99 GCTTATCTACAGCAGTCTGGGCTGAGCTGGAGGCTGGGCTCAGTGAAGTGTCC 158  
 QY 61 GCTTATCTACAGCAGTCTGGGCTGAGCTGGAGGCTGGGCTCAGTGAAGTGTCC 120  
 DB 159 TGCAGGCTTCTGGCTACATTTACAGTATGACATGACTGGTAAAGCAGACCT 218  
 QY 121 TGCAGGCTTCTGGCTACATTTACAGTATGACATGACTGGTAAAGCAGACCT 180  
 DB 219 AGACAGGCGCTGGAATGATGAGACTTTATTCAGAGAAATGATGATCTCTACAT 278  
 QY 181 GACAGGCGCTGGAATGATGAGAAATTTTCTGGAATGATGATCTCTACAT 240  
 DB 279 CAGAGTTCAAGGCGCAAGCCCACTGACTGATGAGCAATCTCCAGCAGACCTACATG 338

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 Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
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 DB 99 GCTTATCTACAGCAGTCTGGGCTGAGCTGGAGGCTGGGCTCAGTGAAGTGTCC 158  
 QY 61 GCTTATCTACAGCAGTCTGGGCTGAGCTGGAGGCTGGGCTCAGTGAAGTGTCC 120  
 DB 159 TGCAGGCTTCTGGCTACATTTACAGTATGACATGACTGGTAAAGCAGACCT 218  
 QY 121 TGCAGGCTTCTGGCTACATTTACAGTATGACATGACTGGTAAAGCAGACCT 180  
 DB 219 AGACAGGCGCTGGAATGATGAGACTTTATTCAGAGAAATGATGATCTCTACAT 278  
 QY 181 GACAGGCGCTGGAATGATGAGAAATTTTCTGGAATGATGATCTCTACAT 240  
 DB 279 CAGAGTTCAAGGCGCAAGCCCACTGACTGATGAGCAATCTCCAGCAGACCTACATG 338

QY 241 CAGAGTTCAAGGCGCAAGCCCTCATGACTGACAGACATCTCCAGCAGACCTACATG 300  
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 QY 301 CAGATCAGACGCTGACATCTGAGACTCTGCGGTCTATTTCTGTGCAAG 352

RESULT 3  
 LOCUS 105921 458 bp PAT 14-NOV-1994  
 DEFINITION Sequence 37 from Patent EP 0274394.  
 ACCESSION 105921  
 NID 9590876  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 458)  
 AUTHORS Robinson, R.R., Liu, A.Y., Hellstrom, K.E., Hellstrom, I. and Ledbetter, J.A.  
 TITLE Chimeric antibody with specificity to human B cell surface antigen  
 JOURNAL Patent: EP 0274394-A2 37 13-JUL-1988;  
 FEATURES  
 source Location/Qualifiers  
 1..458  
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BASE COUNT 113 a 120 c 112 g 113 t  
 ORIGIN  
 Query Match 68.1%; Score 314; DB 22; Length 458;  
 Best Local Similarity 94.6%; Pred. No. 2,71e-216;  
 Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
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 QY 1 ATGGATGAGCTGGGTCTTCTCTCTCTCTGTCATATACAGGTGTCACATCCAG 60  
 DB 99 GCTTATCTACAGCAGTCTGGGCTGAGCTGGAGGCTGGGCTCAGTGAAGTGTCC 158  
 QY 61 GCTTATCTACAGCAGTCTGGGCTGAGCTGGAGGCTGGGCTCAGTGAAGTGTCC 120  
 DB 159 TGCAGGCTTCTGGCTACATTTACAGTATGACATGACTGGTAAAGCAGACCT 218  
 QY 121 TGCAGGCTTCTGGCTACATTTACAGTATGACATGACTGGTAAAGCAGACCT 180  
 DB 219 AGACAGGCGCTGGAATGATGAGACTTTATTCAGAGAAATGATGATCTCTACAT 278  
 QY 181 GACAGGCGCTGGAATGATGAGAAATTTTCTGGAATGATGATCTCTACAT 240  
 DB 279 CAGAGTTCAAGGCGCAAGCCCACTGACTGATGAGCAATCTCCAGCAGACCTACATG 338  
 QY 241 CAGAGTTCAAGGCGCAAGCCCTCATGACTGAGCAGACATCTCCAGCAGACCTACATG 300  
 DB 339 CAGCTCAGACGCTGACATCTGAGACTCTGCGGTCTATTTCTGTGCAAG 390  
 QY 301 CAGATCAGACGCTGACATCTGAGACTCTGCGGTCTATTTCTGTGCAAG 352

RESULT 4  
 LOCUS 108811 458 bp PAT 14-NOV-1994  
 DEFINITION Sequence 12 from Patent WO 8804936.  
 ACCESSION 108811  
 NID 9588489  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 458)  
 AUTHORS Robinson, R.R., Liu, A.Y., Hellstrom, K.E., Hellstrom, I. and Ledbetter, J.A.  
 TITLE Patent: WO 8804936-A 12 14-JUL-1988;  
 JOURNAL Location/Qualifiers  
 FEATURES  
 source Location/Qualifiers  
 1..458  
 /organism="unknown"

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WORLDWIDE (TM)

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Distribution rights by Oxford Molecular Ltd

MPearch\_pp protein - protein database search, using Smith-Waterman algorithm  
on: Thu Apr 15 17:57:49 1999; Maspar time 8.66 Seconds  
627.099 Million cell updates/sec  
Output not generated.

Title: US-08-836-455-2  
Description: (1-145) from US08836455.pep  
Perfect Score: 1019  
Sequence: 1 MGAPAOILGFLLLPGRRC.....IKRADAPTVSIPPPSKLG 145

Scoring table: PAM 150  
Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r58  
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 42.409; Variance 104.536; scale 0.406

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	686	67.3	234	2	SL4237	1.87e-90
5	670	65.8	129	2	D32513	8.40e-88
6	647	63.5	106	2	PL0262	5.39e-84
7	645	63.3	117	1	KVMS3B	1.15e-83
8	640	62.8	234	2	S01320	7.74e-83
9	632	62.0	129	2	S40369	1.62e-81
10	622	61.0	125	2	S40353	7.25e-80
11	622	61.0	141	2	A49134	7.25e-80
12	619	60.7	230	2	S33161	2.26e-79
13	615	60.4	123	2	S40313	1.03e-78
14	615	60.4	129	2	B23986	1.03e-78
15	614	60.3	98	2	PH1062	1.51e-78
16	614	60.3	108	4	B47271	1.51e-78
17	612	60.1	128	4	A26406	3.23e-78
18	610	59.9	129	2	S40317	6.89e-78
19	609	59.8	132	2	S40334	1.01e-77
20	607	59.6	127	2	PH1224	2.15e-77
21	601	59.0	125	2	S40347	2.09e-76
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23	598	58.7	130	2	S40368	6.50e-76

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27	588	57.7	127	2	S40367	2.86e-74
28	586	57.5	122	2	A29380	6.10e-74
29	586	57.5	125	2	S40333	6.10e-74
30	584	57.3	131	2	S40352	1.30e-73
31	583	57.2	115	2	JL0080	1.30e-73
32	583	57.2	129	2	S52793	1.30e-73
33	583	57.2	129	2	S52789	1.30e-73
34	582	57.1	136	2	S40365	1.30e-73
35	582	57.1	126	2	S40335	1.30e-73
36	581	57.0	128	1	KVMS71	4.04e-73
37	580	56.9	88	2	PL0261	5.89e-73
38	580	56.9	129	2	S40332	5.89e-73
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40	578	56.7	128	2	PL0101	1.25e-72
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## ALIGNMENTS

## RESULT 1

ENTRY KVMSM4 #type complete  
TITLE Ig kappa chain precursor V region (MORC 41) - mouse  
CONTAINS Ig kappa chain precursor V region VK41  
ORGANISM Mus musculus #common\_name house mouse  
DATE 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 16-Aug-1996

ACCESSIONS A93211; B93211; A93815; A94239; A01922; A01923

## REFERENCE

#authors Seidman, J.G.; Max, E.E.; Leder, P.  
#journal Nature (1979) 280:370-375  
#title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.  
#accession A93211  
#cross-references MUID:79221900

#molecule\_type DNA

#residues 1-130 #label PC41

#accession B93211

#molecule\_type DNA  
#residues 1-117 #label VK41  
the sequences were determined from the differentiated gene MORC 41 and the germline gene VK41

## REFERENCE

#authors Birstein, Y.; Schechter, I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720  
#title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and kappa-type light chains.  
#accession A93815  
#cross-references MUID:77148916

#molecule\_type protein

#residues 1-33 #label BUR  
Met-3 is apparently used as an alternative initiator in 25% of the chains

## REFERENCE

#authors Gray, W.R.; Dreyer, W.J.; Hood, L.  
#journal Science (1967) 155:465-467  
#title Mechanism of antibody synthesis: size differences between mouse kappa chains.  
#cross-references MUID:67056897

#accession A94239

#molecule\_type protein

#residues 23-49, 'B', '51-53', 'LSB', '57-58', 'ZZ', '61-62', 'BZ', '65-76', 'B', '78-108', '110-130' #label GRA

#experimental\_source Bence Jones protein MORC 41

GENETICS 19/1

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COMPLEX

An immunoglobulin heterotrimer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS alternative initiators; heterotrimer; immunoglobulin

FEATURE 1-22

3-22 #domain signal sequence #status experimental #label SIG1

23-130 #domain signal sequence #status experimental #label SIG2

38-112 #product Ig kappa chain V region (MOPC 41) #status experimental #label M41

45-110 #domain immunoglobulin homology #label IMM

SUMMARY #disulfide bonds #status predicted

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Qy 1 MGARQIGFLIFGGRCDIQMTQSPSSLSASLGERSLTCASQDIGSLNMLQOEP 60

Db 63 DGTIRLIYATSSLDGSGVPRKFSRSGSDSLTSSLESEDFVYICLQYATSPWTFGG 122

Qy 61 DGTIRLIYATSSLDGSGVPRKFSRSGSDSLTSSLESEDFVYICLQYATSPWTFGG 120

Db 123 GTRKEIR 130

Qy 121 GTRKEIR 128

RESULT 2

ENTRY P10260 #type fragment

TITLE Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)

ORGANISM Mus musculus #common\_name house mouse

DATE 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

ACCESSION P10260

REFERENCE P10231

#authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, J. Exp. Med. (1990) 171:265-297

#journal D.; Marshak-Rothstein, A.; Weigert, M.

#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

#cross-references MIMD:90111618

CLASSIFICATION #molecule-type mRNA

KEYWORDS #residues 1-106 #label SHL

FEATURE #superfamily immunoglobulin V region; immunoglobulin homology

1-23 #region framework 1\

24-34 #region complementarity-determining 1\

35-49 #region framework 2\

50-56 #region complementarity-determining 2\

57-88 #region framework 3\

89-97 #region complementarity-determining 3\

98-106 #region framework 4

SUMMARY #length 106 #checksum 2157

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Qy 21 D1QMTQSPSSLSASLGERSLTCASQDIGSLNMLQOEPDGTIRLIYATSSLDGVPK 80

Db 61 RFGSGRSGSDSLTSSLESEDFVYICLQYATSPWTFGGTKLEI 106

Qy 81 RFGSGRSGSDSLTSSLESEDFVYICLQYATSPWTFGGTKLEI 126

RESULT 3

ENTRY P10259 #type fragment

TITLE Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)

ORGANISM Mus musculus #common\_name house mouse

DATE 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

ACCESSION P10259

REFERENCE P10231

#authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, J. Exp. Med. (1990) 171:265-297

#journal D.; Marshak-Rothstein, A.; Weigert, M.

#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

#cross-references MIMD:90111618

CLASSIFICATION #molecule-type mRNA

KEYWORDS #residues 1-106 #label SHL

FEATURE #superfamily immunoglobulin V region; immunoglobulin homology

1-23 #region framework 1\

24-34 #region complementarity-determining 1\

35-49 #region framework 2\

50-56 #region complementarity-determining 2\

57-88 #region framework 3\

89-97 #region complementarity-determining 3\

98-106 #region framework 4

SUMMARY #length 106 #checksum 2162

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Qy 21 D1QMTQSPSSLSASLGERSLTCASQDIGSLNMLQOEPDGTIRLIYATSSLDGVPK 80

Db 61 RFGSGRSGSDSLTSSLESEDFVYICLQYATSPWTFGGTKLEI 106

Qy 81 RFGSGRSGSDSLTSSLESEDFVYICLQYATSPWTFGGTKLEI 126

RESULT 4

ENTRY S14237 #type complete

TITLE Ig kappa chain precursor (15C5) - mouse

ORGANISM Mus musculus #common\_name house mouse

DATE 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Sep-1997

ACCESSION S14237

REFERENCE S14236

#authors Vandamme, A.M.; Bulens, F.; Bernat, H.; Nelles, L.; Ilijen, R.H.; Collen, D.

#journal Eur. J. Biochem. (1990) 192:767-775

#title Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.

#cross-references MIMD:91006173

CLASSIFICATION #molecule-type mRNA

KEYWORDS #residues 1-234 #label VAN

FEATURE #superfamily immunoglobulin V region; immunoglobulin homology

1-234 #region framework 1\

235-268 #region complementarity-determining 1\

269-292 #region framework 2\

293-316 #region complementarity-determining 2\

317-340 #region framework 3\

341-364 #region complementarity-determining 3\

365-388 #region framework 4

SUMMARY #length 388 #checksum 6000

Query Match 67.3%; Score 686; DB 2; Length 234; Best Local Similarity 69.0%; Pred. No. 1,876-90; Matches 98; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

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 W O R L D  
 (TM)  
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 Search: protein - protein database search, using Smith-Waterman algorithm  
 on: Tue Mar 23 15:01:25 1999; Maspar time 2.89 Seconds  
 61.491 Million cell updates/sec

Tabular output not generated.

Title: >US-08-766-350A-2  
 Description: (24-34) from US08766350A.pep (2 of 4)  
 Perfect Score: 63  
 Sequence: 1 MTQSPSSLSAS 11

Scoring table: PAM 150  
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database:

a-geneseq32  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23  
 24:part24 25:part25 26:part26 27:part27 28:part28  
 29:part29

Statistics: Mean 15.144; Variance 52.220; scale 0.290

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	63	100.0	104	29	W52225	Antibody LD2-4-VL cha	3.52e+00
2	63	100.0	105	29	W52217	Antibody LD1-84-VL ch	3.52e+00
3	63	100.0	105	29	W52239	Antibody LD1-6-17-VL	3.52e+00
4	63	100.0	105	29	W52241	Antibody LD1-2-6-3-VL	3.52e+00
5	63	100.0	105	29	W52219	Antibody LD1-110-VL c	3.52e+00
6	63	100.0	105	29	W52237	Antibody LD2-20-VL ch	3.52e+00
7	63	100.0	105	29	W52233	Antibody LD2-14-VL ch	3.52e+00
8	63	100.0	106	29	W52213	Antibody LD1-52-VL ch	3.52e+00
9	63	100.0	106	29	W52215	Antibody LD2-5-VL cha	3.52e+00
10	63	100.0	106	29	W52227	Antibody LD1-117-VL c	3.52e+00
11	63	100.0	106	29	W52221	Antibody LD1-117-VL c	3.52e+00
12	63	100.0	106	29	W52217	Antibody LD2-5-VL cha	3.52e+00
13	63	100.0	107	29	W41390	Humanised alpha-4 int	3.52e+00
14	63	100.0	107	29	W41397	Anti-CEA antibody 11g	3.52e+00
15	63	100.0	107	29	W23953	Anti-CEA antibody 806	3.52e+00
16	63	100.0	107	29	W4123	Chimeric humanised Mu	3.52e+00
17	63	100.0	107	27	W27568	Light chain variable	3.52e+00
18	63	100.0	107	21	W11920	Anti-TNF-alpha antibo	3.52e+00
						Humanised MAb SK48-52	3.52e+00

19	63	100.0	107	14	R79247	Light chain variable	3.52e+00
20	63	100.0	107	14	R78972	Light chain variable	3.52e+00
21	63	100.0	108	27	W23440	Modified light chain	3.52e+00
22	63	100.0	108	27	W23439	Modified light chain	3.52e+00
23	63	100.0	108	27	W23442	Variant variable light	3.52e+00
24	63	100.0	108	21	W04177	Light chain variable	3.52e+00
25	63	100.0	108	5	R28751	Interleukin-5 humanis	3.52e+00
26	63	100.0	113	29	W42472	Human V kappa65.15 fra	3.52e+00
27	63	100.0	117	28	W41147	Humanised light chain	3.52e+00
28	63	100.0	126	28	W31664	Human/murine chimeric	3.52e+00
29	63	100.0	126	14	R76678	Human/murine chimeric	3.52e+00
30	63	100.0	126	14	R76675	Human/murine chimeric	3.52e+00
31	63	100.0	126	14	R76676	Human/murine chimeric	3.52e+00
32	63	100.0	126	14	R76680	Human/murine chimeric	3.52e+00
33	63	100.0	126	14	W04388	Human/murine chimeric	3.52e+00
34	63	100.0	126	27	W31691	Humanised anti-VLA-4	3.52e+00
35	63	100.0	128	18	R90684	Humanized SC7.29 anti	3.52e+00
36	63	100.0	214	26	W34504	Light chain of full 1	3.52e+00
37	63	100.0	214	26	W34506	Human anti-RSV monocl	3.52e+00
38	63	100.0	234	21	W11638	Humanised light chain	3.52e+00
39	63	100.0	235	29	W41611	Humanised antibody 80	3.52e+00
40	63	100.0	235	29	W41398	Human anti-RSV monocl	3.52e+00
41	63	100.0	235	21	W11640	Chimeric humanised Mu	3.52e+00
42	63	100.0	240	29	W23954	Humanised anti-CD38 m	3.52e+00
43	63	100.0	245	19	R98943	R. papiens recombinan	3.52e+00
44	63	100.0	355	28	W35133		
45	63	100.0					

#### ALIGNMENTS

\*\*\*\*\*  
 1  
 ID W52225 standard; Protein; 104 AA.  
 AC W52225;  
 DT 12-JUN-1998 (first entry)  
 DE Antibody LD2-4-VL chain sequence.  
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;  
 KM Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.  
 OS Homo sapiens.  
 PN W09749809-A1.  
 PD 31-DEC-1997.  
 PE 20-JUN-1997; E03253.  
 PR 24-JUN-1996; EP-810421.  
 PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.  
 PI Ametutz H, Imboden M, Miescher S, Morell A, Stadler B,  
 PI Vogel M;  
 DR WPI; 98-077173/07.  
 DR N-PSDB; V19749.  
 PT New Rhesus D antigen binding poly(peptide(s) - used to neutralise  
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic  
 PT thrombocytopenic purpura.  
 PS Claim 1; Fig 7B; 68pp; English.  
 CC This sequence is the antibody LD2-4-VL chain sequence, which is a  
 CC polypeptide of the invention. The polypeptides are capable of forming  
 CC antigen binding structures with specificity for Rhesus D antigens which  
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
 CC variable heavy (VH) and variable light (VL) chain sequences. The  
 CC antibodies are active against the Rhesus D antigen. They can be used for  
 CC treating disorders which would benefit from anti-rhesus D immunoglobulin,  
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
 CC protection of Rhesus negative women before or immediately after the birth  
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn  
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D  
 CC immunoglobulin can be used after transfusions of Rhesus positive blood  
 CC to Rhesus negative recipients in order to prevent sensitisation to the  
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
 CC Sequence 104 AA:  
 Query Match 100.0%; Score 63; DB 29; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; \*

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PD 31-DEC-1997. E03253.  
 PF 20-JUN-1997; EP-810421.  
 PR 24-JUN-1996; EP-810421.  
 PA (ROK-) ROKKREUZSTIFTUNG ZENT LAB BUTTSPENDE.  
 PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,  
 PI Vogel M;  
 DR WPI: 98-077173/07.  
 DR N-PSDB: V19745.  
 PT New Rhesus D antigen binding polypeptide(s) - used to neutralise  
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic  
 PT thrombocytopenic purpura  
 PS Claim 1: Fig 5B; 68pp; English.  
 CC This sequence is the antibody LD1-117-VL chain sequence, which is a  
 CC polypeptide of the invention. The polypeptides are capable of forming  
 CC antigen binding structures with specificity for Rhesus D antigens which  
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of  
 CC variable heavy (VH) and variable light (VL) chain sequences. The  
 CC antibodies are active against the Rhesus D antigen. They can be used for  
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,  
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the  
 CC protection of Rhesus negative women before or immediately after the birth  
 CC of a Rhesus positive child to prevent hemolytic disease of the newborn  
 CC (HUN) in subsequent pregnancies. In addition, anti-Rhesus D  
 CC immunoglobulin can be used after transfusions of Rhesus positive blood  
 CC to Rhesus negative recipients in order to prevent sensitisation to the  
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.  
 SO Sequence 106 AA;

Query Match 100.0%; Score 63; DB 29; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 mtgspsslsas 12  
 |||||  
 24 MTGSPSSLSAS 34

RESULT 12  
 ID W22412 standard; Protein; 106 AA.  
 AC W22412;  
 DT 08-DEC-1997 (first entry)  
 DE Humanised alpha-4 integrin antibody 21.6 VL Ia.  
 KM Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;  
 KM asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;  
 KM metastasis; inflammatory bowel disease; rheumatoid arthritis;  
 KM transplant rejection; graft versus host disease; nephritis;  
 KM atopic dermatitis; psoriasis; myocardial ischemia;  
 KM acute leukocyte mediated lung injury; therapy.  
 KM Chimeric Mus musculus;  
 CC Chimeric Homo sapiens;  
 CC Chimeric synthetic.  
 FH Key  
 FT location/Qualifiers  
 FT 1..23  
 FT region  
 FT /label= FR1  
 FT /note= "REI framework region 1"  
 FT 24..34  
 FT region  
 FT /label= CDR1  
 FT /note= "21.6 complementarity determining region 1"  
 FT 35..49  
 FT region  
 FT /label= FR2  
 FT /note= "REI framework region 2"  
 FT misc-difference 45  
 FT /note= "REI Lys-45 is subst. by Lys of mouse  
 FT 21.6 VL, important in supporting the  
 FT CDR2 loop"  
 FT 49  
 FT /note= "REI Tyr-49 is subst. by His of mouse  
 FT 21.6 VL, located at the binding site"  
 FT misc-difference 45  
 FT /note= "REI Lys-45 is subst. by Lys of mouse  
 FT 21.6 VL, located at the binding site"  
 FT 50..56  
 FT region  
 FT /label= CDR2  
 FT /note= "21.6 complementarity determining region 2"  
 FT 57..88  
 FT region  
 FT /label= FR3

FT /note= "REI framework region 3"  
 FT misc-difference 58  
 FT /note= "REI Val-58 is subst. by Ile of mouse  
 FT 21.6 VL, important in supporting the CDR2  
 FT loop"  
 FT misc-difference 69  
 FT /note= "REI Thr-69 is subst. by Arg of mouse  
 FT 21.6 VL, involved in antibody-antigen  
 FT binding"  
 FT 89..96  
 FT region  
 FT /label= CDR3  
 FT /note= "21.6 complementarity determining region 3"  
 FT 97..106  
 FT region  
 FT /label= FR4  
 FT /note= "REI framework region 4"  
 FT misc-difference 103  
 FT /note= "REI Leu-103 subst. by Val, more typical  
 FT of human kappa light chain J region"  
 FT misc-difference 104  
 FT /note= "REI Gln-104 subst. by Glu, more typical  
 FT of human kappa light chain J region"  
 FT misc-difference 106  
 FT /note= "REI Thr-106 subst. by Lys, more typical  
 FT of human kappa light chain J region"  
 FT PN W09718838-A1.  
 PD 29-MAY-1997.  
 PF 21-NOV-1996; U18807.  
 PR 21-NOV-1995; US-561521.  
 PA (ATHE-) ATHENA NEUROSCIENCES INC.  
 PI Bondy KM, Jones ST, Leger OJ, Saldanha J, Yednock TA;  
 DR WPI: 97-297879/27.  
 PT Uses of humanised alpha-4 integrin antibody - for treatment of  
 PT asthma, atherosclerosis, AIDS, dementia, etc.  
 PS Claim 25; Fig 6; 107pp; English.  
 CC This polypeptide, designated Ia, comprises the light chain variable  
 CC region (VL) of a humanised alpha-4 integrin antibody 21.6. It is  
 CC composed of complementarity determining regions (CDRs) from the VL  
 CC region (see W22409) of mouse alpha-4 integrin monoclonal antibody  
 CC 21.6 and a modified human REI framework. It can be expressed in  
 CC mammalian host cells following PCR amplification and mutagenesis  
 CC of appropriate fragments of mouse and human DNA sequences. The  
 CC humanised 21.6 VL and a humanised 21.6 VH (see W22413) can be used  
 CC to produce a claimed humanised 21.6 antibody that is useful in the  
 CC manufacture of a medicament for treating asthma, atherosclerosis,  
 CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid  
 CC arthritis, transplant rejection, graft versus host disease, tumour  
 CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial  
 CC ischemia, and acute leukocyte mediated lung injury. The antibody  
 CC may also be used in the affinity purification of alpha-4 integrin  
 CC for use as a vaccine or an immunogen. It is also useful for  
 CC generating idiotypic antibodies. The humanised antibody has a  
 CC half-life in the human circulation essentially equivalent to that  
 CC of naturally occurring human antibodies.  
 SO Sequence 106 AA;

Query Match 100.0%; Score 63; DB 24; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 mtgspsslsas 14  
 |||||  
 24 MTGSPSSLSAS 34

RESULT 13  
 ID W41390 standard; Protein; 107 AA.  
 AC W41390;  
 DT 02-JUN-1998 (first entry)  
 DE Anti-CEA antibody light chain variable region VK4.  
 KM Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;  
 KM cancer diagnosis; complementarity determining region; light chain.  
 OS Synthetic.  
 PN W09743329-A1.

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
on: Tue Mar 23 15:20:39 1999; Maspar time 1.37 Seconds  
Molecular output not generated. 34.477 Million cell updates/sec

Title: >US-08-766-350A-4  
Description: (31-35) from US08766350A.pep (2 of 4)  
Perfect Score: 31  
Sequence: 1 VRSGA 5

Scoring table: PAM 150  
Gap 11

Searched: 100342 seqs, 9469514 residues

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfile1

Statistics: Mean 11.797; Variance 23.980; scale 0.492

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	31	100.0	124	2	US-08-471-	Sequence 6, Applicatio	1.86e+02	
2	31	100.0	124	1	US-08-017-	Sequence 4, Applicatio	1.86e+02	
3	31	100.0	124	2	US-08-471-	Sequence 4, Applicatio	1.86e+02	
4	31	100.0	124	3	PCT-US94-0	Sequence 6, Applicatio	1.86e+02	
5	31	100.0	124	1	US-08-017-	Sequence 6, Applicatio	1.86e+02	
6	31	100.0	124	3	PCT-US94-0	Sequence 6, Applicatio	1.86e+02	
7	31	100.0	221	2	US-08-342-	Sequence 5, Applicatio	1.86e+02	
8	31	100.0	341	1	US-08-314-	Sequence 19, Applicati	1.86e+02	
9	31	100.0	386	2	US-08-663-	Sequence 6, Applicatio	1.86e+02	
10	31	100.0	484	1	US-08-482-	Sequence 26, Applicati	1.86e+02	
11	31	100.0	484	1	US-08-127-	Sequence 26, Applicati	1.86e+02	
12	31	100.0	659	1	US-08-116-	Sequence 3, Applicatio	1.86e+02	
13	31	100.0	659	2	US-08-479-	Sequence 3, Applicatio	1.86e+02	
14	31	100.0	691	3	PCT-US91-0	Sequence 2, Applicatio	1.86e+02	
15	29	93.5	73	2	US-08-379-	Sequence 7, Applicatio	3.70e+02	
16	29	93.5	185	4	5514590-10	Patent No. 5514590.	3.70e+02	
17	29	93.5	185	1	US-08-278-	Sequence 14, Applicati	3.70e+02	
18	29	93.5	185	1	US-08-483-	Sequence 14, Applicati	3.70e+02	
19	29	93.5	185	1	US-08-472-	Sequence 14, Applicati	3.70e+02	
20	29	93.5	185	2	US-08-487-	Sequence 14, Applicati	3.70e+02	
21	29	93.5	299	4	5514590-4	Patent No. 5514590.	3.70e+02	
22	29	93.5	396	2	US-08-926-	Sequence 2, Applicatio	3.70e+02	
23	29	93.5	421	2	US-07-955-	Sequence 27, Applicati	3.70e+02	

24	29	93.5	471	3	PCT-US95-0	Sequence 2, Applicatio	3.70e+02
25	29	93.5 <td>516</td> <td>1<th>US-08-356-</th><th>Sequence 4, Applicatio</th><th>3.70e+02</th></td>	516	1 <th>US-08-356-</th> <th>Sequence 4, Applicatio</th> <th>3.70e+02</th>	US-08-356-	Sequence 4, Applicatio	3.70e+02
26	29	93.5 <td>559</td> <td>2<th>US-08-661-</th><th>Sequence 16, Applicati</th><th>3.70e+02</th></td>	559	2 <th>US-08-661-</th> <th>Sequence 16, Applicati</th> <th>3.70e+02</th>	US-08-661-	Sequence 16, Applicati	3.70e+02
27	29	93.5 <td>1018</td> <td>1<th>US-08-406-</th><th>Sequence 20, Applicati</th><th>3.70e+02</th></td>	1018	1 <th>US-08-406-</th> <th>Sequence 20, Applicati</th> <th>3.70e+02</th>	US-08-406-	Sequence 20, Applicati	3.70e+02
28	29	93.5 <td>1018</td> <td>1<th>US-08-714-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-714-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-08-714-	Sequence 6, Applicatio	3.70e+02
29	29	93.5 <td>1018</td> <td>1<th>US-08-452-</th><th>Sequence 2, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-452-</th> <th>Sequence 2, Applicatio</th> <th>3.70e+02</th>	US-08-452-	Sequence 2, Applicatio	3.70e+02
30	29	93.5 <td>1018</td> <td>1<th>US-08-408-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-408-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-08-408-	Sequence 6, Applicatio	3.70e+02
31	29	93.5 <td>1018</td> <td>1<th>US-08-408-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-408-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-08-408-	Sequence 6, Applicatio	3.70e+02
32	29	93.5 <td>1045</td> <td>1<th>US-07-783-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1045	1 <th>US-07-783-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-07-783-	Sequence 6, Applicatio	3.70e+02
33	29	93.5 <td>1045</td> <td>1<th>US-07-934-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1045	1 <th>US-07-934-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-07-934-	Sequence 6, Applicatio	3.70e+02
34	29	93.5 <td>1045</td> <td>1<th>US-07-596-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1045	1 <th>US-07-596-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-07-596-	Sequence 6, Applicatio	3.70e+02
35	28	90.3 <td>275</td> <td>4<th>5472855-4</th><th>Patent No. 5472855.</th><th>5.19e+02</th></td>	275	4 <th>5472855-4</th> <th>Patent No. 5472855.</th> <th>5.19e+02</th>	5472855-4	Patent No. 5472855.	5.19e+02
36	28	90.3 <td>380</td> <td>4<th>RE34606-2</th><th>Patent No. RE34,606.</th><th>5.19e+02</th></td>	380	4 <th>RE34606-2</th> <th>Patent No. RE34,606.</th> <th>5.19e+02</th>	RE34606-2	Patent No. RE34,606.	5.19e+02
37	28	90.3 <td>616</td> <td>2<th>US-08-638-</th><th>Sequence 35, Applicati</th><th>5.19e+02</th></td>	616	2 <th>US-08-638-</th> <th>Sequence 35, Applicati</th> <th>5.19e+02</th>	US-08-638-	Sequence 35, Applicati	5.19e+02
38	28	90.3 <td>774</td> <td>1<th>US-07-747-</th><th>Sequence 5, Applicatio</th><th>5.19e+02</th></td>	774	1 <th>US-07-747-</th> <th>Sequence 5, Applicatio</th> <th>5.19e+02</th>	US-07-747-	Sequence 5, Applicatio	5.19e+02
39	28	90.3 <td>774</td> <td>1<th>US-08-019-</th><th>Sequence 5, Applicatio</th><th>5.19e+02</th></td>	774	1 <th>US-08-019-</th> <th>Sequence 5, Applicatio</th> <th>5.19e+02</th>	US-08-019-	Sequence 5, Applicatio	5.19e+02
40	28	90.3 <td>780</td> <td>2<th>US-08-786-</th><th>Sequence 14, Applicati</th><th>5.19e+02</th></td>	780	2 <th>US-08-786-</th> <th>Sequence 14, Applicati</th> <th>5.19e+02</th>	US-08-786-	Sequence 14, Applicati	5.19e+02
41	28	90.3 <td>853</td> <td>2<th>US-08-638-</th><th>Sequence 27, Applicati</th><th>5.19e+02</th></td>	853	2 <th>US-08-638-</th> <th>Sequence 27, Applicati</th> <th>5.19e+02</th>	US-08-638-	Sequence 27, Applicati	5.19e+02
42	28	90.3 <td>853</td> <td>2<th>US-08-638-</th><th>Sequence 31, Applicati</th><th>5.19e+02</th></td>	853	2 <th>US-08-638-</th> <th>Sequence 31, Applicati</th> <th>5.19e+02</th>	US-08-638-	Sequence 31, Applicati	5.19e+02
43	28	90.3 <td>1958</td> <td>1<th>US-07-945-</th><th>Sequence 2, Applicatio</th><th>5.19e+02</th></td>	1958	1 <th>US-07-945-</th> <th>Sequence 2, Applicatio</th> <th>5.19e+02</th>	US-07-945-	Sequence 2, Applicatio	5.19e+02
44	28	90.3 <td>2842</td> <td>1<th>US-08-289-</th><th>Sequence 2, Applicatio</th><th>5.19e+02</th></td>	2842	1 <th>US-08-289-</th> <th>Sequence 2, Applicatio</th> <th>5.19e+02</th>	US-08-289-	Sequence 2, Applicatio	5.19e+02
45	28	90.3 <td>2873</td> <td>2<th>US-08-638-</th><th>Sequence 2, Applicatio</th><th>5.19e+02</th></td>	2873	2 <th>US-08-638-</th> <th>Sequence 2, Applicatio</th> <th>5.19e+02</th>	US-08-638-	Sequence 2, Applicatio	5.19e+02

## ALIGNMENTS

RESULT 1 STANDARD; PRT; 124 AA.

US-08-471-426-6

xxxxxx

Sequence 6, Application US/08471426

Sequence 6, Application US/08471426

Patent No. 5808033

GENERAL INFORMATION:

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLON, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,426

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/017,570

FILING DATE: 16-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

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**THIS PAGE BLANK (USPTO)**

CC LENGTH: 124 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 124 AA; 13816 MW; 93186 CN;

Query Match 100.0%; Score 31; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.86e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 VRSGA 16  
|  
|  
|  
|  
OY 31 VRSGA 35

RESULT 2  
ID US-08-017-570-4 STANDARD: PRT; 124 AA.  
xxxxxx

Sequence 4, Application US/08017570

Sequence 4, Application US/08017570  
Patent No. 5472693

GENERAL INFORMATION:

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/017,570

FILING DATE: 19930216

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 124 AA; 13786 MW; 91250 CN;

Query Match 100.0%; Score 31; DB 1; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.86e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 VRSGA 16  
|  
|  
|  
|  
OY 31 VRSGA 35

RESULT 3  
ID US-08-471-426-4 STANDARD: PRT; 124 AA.  
xxxxxx

Sequence 4, Application US/08471426

Sequence 4, Application US/08471426  
Patent No. 5808033

GENERAL INFORMATION:

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,426

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/017,570

FILING DATE: 16-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 124 AA; 13786 MW; 91250 CN;

Query Match 100.0%; Score 31; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.86e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 VRSGA 16  
|  
|  
|  
|  
OY 31 VRSGA 35

RESULT 4  
ID PCT-US94-01709-6 STANDARD: PRT; 124 AA.  
xxxxxx  
Sequence 6, Application PC/TUS9401709  
Sequence 6, Application PC/TUS9401709

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